

SEQUENCE LISTING

RECEIVED

NOV 16 2000



TECH CENTER 1600/2900

<110> Cortes, J
Fromentin, C
Gaisser, S
Leadlay, P
Mendez, C
Michel, J-M
Raynal, M-C
Salah-Bey, K
Salas, J

<120> BIOSYNTHESIS GENES & TRANSFER OF 6-DESOXYHEXOSES IN
SACCHAROPOLYSPORA ERYTHRAEA AND IN STREPTOMYCES
ANTIBIOTICUS AND THEIR USE

<130> 146.1335

<140> 09/463705

<141> 2000-02-23

<150> PCT/FR98/01593

<151> 1998-07-21

<150> 98/07411

<151> 1988-06-12

<150> 97/09458

<151> 1997-07-25

<160> 61

<170> PatentIn Ver. 2.1

<210> 1

<211> 3439

<212> DNA

<213> Saccharopolyspora erythraea

<220>

<221> CDS

<222> Complement((48)..(1046))

<223> /function= "involved in the biosynthesis of
mycarose" /gene= "eryBII"

<220>

<221> CDS

<222> Complement((2322)..(3404))

<223> /function= "involved in the biosynthesis of
desosamine" /gene= "eryCII"

<400> 1

gcttcacgct caccagccgt atcctttctc ggttcctctt gtgctcactg caaccaggct 60

tccggcgccg cgccgccgga ggccaccgcg gggaagatct cgtccagttc ggacagcgcc 120

tgctcgcca gggatcatgc ggaagccttc agcgcgaggt cgagctgctc ggggggttcgc 180

gggccgatga cggcgccggc gatgccgggc cgggacagca cccatgagag cccacactcg 240
 gccgggtctt cgccgaggtt gcggcagaac ttctcgtagg cctcgatcgc cgggagcagg 300
 gacggcaaca gcacctgcgc acggccctgc gccgacttca ccgcggtgcc cgcggccagc 360
 ttctccagcg ctccgctgag caggccgcgc tgcagcggcg accaggcgaa gacgccgagc 420
 ccgtaggcct gcgcggcggg cagcacctcc agctcggcgt gccggaccgc caggttgtag 480
 aggcactggt gggagaccat gcccaggag tggcgccggg cggcggttct ctgcgcggcg 540
 gcgatgtgcc agcccgcgaa gttcgacgag ccgacgtagg agacctgcc gctggcgacg 600
 aggtgtcca tggcctgcc cacctcgtec caccgagcgc accggtcgat gtggtgcatc 660
 tggtagacgt cgatgtggtc gacgcccagc ctgcgcagcg atccctcgca ggaggcgatg 720
 atgtgccgcg ccgacagccc gctgtcggtt acgcgctcgc tcatctcgcc gccgaccttg 780
 gtcgccagca cgggtgtctc gcgcgcgtcc cgcacctggg ccagccacct gccaccagc 840
 tcctcgggtg ggcccttgta gagccgccag ccgtacatgt cggcggtgtc gaggcagttg 900
 atgccgcggt cccgggcgtg gtccatcagg cgcagcgcgt cgtcgtctc gacgcgtccg 960
 ctgaagttca ccgtgccgag ccagagcctg ctggtgagca gcgcggaacg cccgagccgc 1020
 acgtgcgtcg cggcgctcgtt ggtcatcggt gttctctctt tcctgcggcc agttctctcg 1080
 agatgccgac gacctcgcc ggtgacggct ccgcgagcat gtcgtcgcgc atccgcgcgc 1140
 cgccggcgcg gtgggcccgg tcgtcgagga cccgcttcac cgactcccgg agctggtcgg 1200
 gggtcagctc gggcacgggc agcgcgatcc ccgccccgaa tcctgcgtg cgtcgcgcgc 1260
 gcacgccggt gtcccagccg tcgggcagga tcacctgcgc cagccgtgg atcgcgcgcg 1320
 tgtgccagct cccgggtccg ccgtggtgca ccgtcgcgc gcaggtcggc agcagcgcgt 1380
 gcatcgggac gaagccgacc gtgcggacgt tgtccgggat gttcgcgacg ccttctagct 1440
 gctgcgcgtc gaaggtcgcg atgatctcgg cgtcgacgtc gccgacggca cccagcagct 1500
 cctcgatgga gacctgccc atgctgttct cgcggctgga gatcccgagc gtgaggcaca 1560
 cgcgggcgcg ctcggtctcg tcgtgcagcc attccggcac cagggacggc ccgttgtagt 1620
 cgacgtagcg catcccgacg gtcttcaggc cgggtgtcag cctgatcgcg gccggggcgg 1680
 ggtcgatcgt cactgcccg acgaccacct cctcgtcgaa ggccgggccc ccgtacttct 1740
 ccagcgtcca ggtgagccac tcggcgagcg ggtcctccc gtgctcctcc ggctggtcgg 1800
 gcagcaggcc gaggaagttc tgccgcgccc gggtggtgat gtcgggtccc cacagcagcc 1860

gcgcgtgcgg	cgttcgggtc	accgccgccc	cgatgggccc	ggcgaagggtg	agcgggtccc	1920
agatgaccag	gtcggggccc	cacttcgggc	agaacgagac	catgccttcg	atgagcgtgt	1980
ccgggctcat	cagggcgtag	aaggtcgggg	tgagcacggt	ctgcatgccc	agcaggtgct	2040
cccaggtcaa	ggtggcgggg	tcccgtcgc	tgaagtccag	gctccggacg	tagtcgatga	2100
tgtcgtggcc	cgcgtgggtc	atgaagtcca	cgaggtcgac	gtcggtgccg	accgggacgg	2160
cggtcagccc	ggccgcggtg	atgtcctcgg	tgagcgccgg	ggacgcgacc	acgcggacct	2220
cgtgccccgc	cgcgcggaac	gcccattgca	gggggacgag	gccgaagagg	tggctcttgc	2280
tggccatgga	ggagaagacg	acgcgcacgc	cggttacctc	agagctcgac	ggggcagcgg	2340
ttggttcccc	gcaggacggg	tgatcggcgg	cgccggacga	ccgggcccgt	gggcgtgagt	2400
ccgggcagcg	ccttggccgc	ggcccgcagt	gcggcggtgg	cgagcgcggt	gaccagctcc	2460
tccagcctgc	cggggtggcc	gcgatgtgcc	gacagcgccc	ggtcggcgtc	ggggcggtcc	2520
acgtcgaggc	ggtcggggtc	ggcgaagacc	tccgggtcgc	ggttggccgc	cgcgacgacg	2580
accacgacct	cctcgccttc	gcgatcacg	tgctcgccga	gccgcacctc	tgcggtggcc	2640
gtgcgcccgt	ccaggtgcaa	tgccgggtgc	aggcgcagca	cctcggcgac	ggttcgctgc	2700
gcggcgggcg	ggtcgtcggc	gatccgttcg	gccagccccg	gttcggccga	gacggccagg	2760
accgcgtcga	ccacggtggt	cgcgggtcgc	tcgccccggg	cgaacagggc	gcgcagtgcg	2820
gggtcggcgg	gcagtgcgcg	gaccgctgct	tcggtcaccg	cgagctgctg	cgggctgagc	2880
tgggcgtcca	ggctgacgcg	ggcgtcccac	gcggcgccgc	gcagcactcc	ggctgcgccg	2940
agcacggcgg	tcatgccctg	caccggtacc	tgccaggcga	agtcgccgac	caggtccagc	3000
cgcgcgcccc	cgccggggag	cagaccggcg	aagctctccg	ccagttcccc	gacgtcgggg	3060
acctcgcctt	ccagggacgc	ggcgtgcacg	tcccggaaac	gctgggcccc	ctcggcgggg	3120
ggcgcgcccc	cggcccgcct	ccattccggg	gtgcgtccgg	tggcgcgggg	gaacgcgggg	3180
tcgtcgagca	cctgcggggc	ggtggcggtg	tcggccacca	cccacgtctc	ggtgcggctg	3240
cgcgcacac	cggactcgcg	catcgagcgg	taccggcgct	gcgggtcgtc	gtcgtgtccg	3300
cacagcagca	tcgggtaagg	gtcgcggttg	ctgccgtaac	cccagtgcag	gccgcggatc	3360
atctggagct	gcctgcccag	cccggcgcca	tcggtcgtgg	tcatgaattc	cctccgcccc	3420
gccaggcgtc	gatgtgccg					3439

<210> 2
<211> 333

<212> PRT

<213> Saccharopolyspora erythraea

<400> 2

Met	Thr	Thr	Asp	Ala	Ala	Thr	His	Val	Arg	Leu	Gly	Arg	Ser	Ala	Leu
1				5					10					15	
Leu	Thr	Ser	Arg	Leu	Trp	Leu	Gly	Thr	Val	Asn	Phe	Ser	Gly	Arg	Val
			20					25					30		
Glu	Asp	Asp	Asp	Ala	Leu	Arg	Leu	Met	Asp	His	Ala	Arg	Asp	Arg	Gly
		35					40					45			
Ile	Asn	Cys	Leu	Asp	Thr	Ala	Asp	Met	Tyr	Gly	Trp	Arg	Leu	Tyr	Lys
	50					55					60				
Gly	His	Thr	Glu	Glu	Leu	Val	Gly	Arg	Trp	Leu	Ala	Gln	Gly	Gly	Gly
65					70					75					80
Arg	Arg	Glu	Asp	Thr	Val	Leu	Ala	Thr	Lys	Val	Gly	Gly	Glu	Met	Ser
				85					90					95	
Glu	Arg	Val	Asn	Asp	Ser	Gly	Leu	Ser	Ala	Arg	His	Ile	Ile	Ala	Ser
			100					105					110		
Cys	Glu	Gly	Ser	Leu	Arg	Arg	Leu	Gly	Val	Asp	His	Ile	Asp	Val	Tyr
		115					120					125			
Gln	Met	His	His	Ile	Asp	Arg	Ser	Ala	Pro	Trp	Asp	Glu	Val	Trp	Gln
	130					135					140				
Ala	Met	Asp	Ser	Leu	Val	Ala	Ser	Gly	Lys	Val	Ser	Tyr	Val	Gly	Ser
145					150					155					160
Ser	Asn	Phe	Ala	Gly	Trp	His	Ile	Ala	Ala	Ala	Gln	Glu	Asn	Ala	Ala
				165					170					175	
Arg	Arg	His	Ser	Leu	Gly	Met	Val	Ser	His	Gln	Cys	Leu	Tyr	Asn	Leu
			180					185					190		
Ala	Val	Arg	His	Ala	Glu	Leu	Glu	Val	Leu	Pro	Ala	Ala	Gln	Ala	Tyr
		195					200					205			
Gly	Leu	Gly	Val	Phe	Ala	Trp	Ser	Pro	Leu	His	Gly	Gly	Leu	Leu	Ser
	210					215					220				
Gly	Ala	Leu	Glu	Lys	Leu	Ala	Ala	Gly	Thr	Ala	Val	Lys	Ser	Ala	Gln
225					230					235					240
Gly	Arg	Ala	Gln	Val	Leu	Leu	Pro	Ser	Leu	Arg	Pro	Ala	Ile	Glu	Ala
				245					250					255	
Tyr	Glu	Lys	Phe	Cys	Arg	Asn	Leu	Gly	Glu	Asp	Pro	Ala	Glu	Val	Gly
			260					265					270		
Leu	Ala	Trp	Val	Leu	Ser	Arg	Pro	Gly	Ile	Ala	Gly	Ala	Val	Ile	Gly
		275					280					285			

Pro Arg Thr Pro Glu Gln Leu Asp Ser Ala Leu Lys Ala Ser Ala Met
 290 295 300

Thr Leu Asp Glu Gln Ala Leu Ser Glu Leu Asp Glu Ile Phe Pro Ala
 305 310 315 320

Val Ala Ser Gly Gly Ala Ala Pro Glu Ala Trp Leu Gln
 325 330

<210> 3

<211> 361

<212> PRT

<213> Saccharopolyspora erythraea

<400> 3

Met Thr Thr Thr Asp Arg Ala Gly Leu Gly Arg Gln Leu Gln Met Ile
 1 5 10 15

Arg Gly Leu His Trp Gly Tyr Gly Ser Asn Gly Asp Pro Tyr Pro Met
 20 25 30

Leu Leu Cys Gly His Asp Asp Asp Pro Gln Arg Arg Tyr Arg Ser Met
 35 40 45

Arg Glu Ser Gly Val Arg Arg Ser Arg Thr Glu Thr Trp Val Val Ala
 50 55 60

Asp His Ala Thr Ala Arg Gln Val Leu Asp Asp Pro Ala Phe Thr Arg
 65 70 75 80

Ala Thr Gly Arg Thr Pro Glu Trp Met Arg Ala Ala Gly Ala Pro Pro
 85 90 95

Ala Glu Trp Ala Gln Pro Phe Arg Asp Val His Ala Ala Ser Trp Glu
 100 105 110

Gly Glu Val Pro Asp Val Gly Glu Leu Ala Glu Ser Phe Ala Gly Leu
 115 120 125

Leu Pro Gly Ala Gly Ala Arg Leu Asp Leu Val Gly Asp Phe Ala Trp
 130 135 140

Gln Val Pro Val Gln Gly Met Thr Ala Val Leu Gly Ala Ala Gly Val
 145 150 155 160

Leu Arg Gly Ala Ala Trp Asp Ala Arg Val Ser Leu Asp Ala Gln Leu
 165 170 175

Ser Pro Gln Gln Leu Ala Val Thr Glu Ala Ala Val Ala Ala Leu Pro
 180 185 190

Ala Asp Pro Ala Leu Arg Ala Leu Phe Ala Gly Ala Glu Met Thr Ala
 195 200 205

Asn Thr Val Val Asp Ala Val Leu Ala Val Ser Ala Glu Pro Gly Leu

210	215	220
Ala Glu Arg Ile Ala Asp Asp Pro Ala Ala Ala Gln Arg Thr Val Ala		
225	230	235 240
Glu Val Leu Arg Leu His Pro Ala Leu His Leu Glu Arg Arg Thr Ala		
	245	250 255
Thr Ala Glu Val Arg Leu Gly Glu His Val Ile Gly Glu Gly Glu Glu		
	260	265 270
Val Val Val Val Val Ala Ala Ala Asn Arg Asp Pro Glu Val Phe Ala		
	275	280 285
Glu Pro Asp Arg Leu Asp Val Asp Arg Pro Asp Ala Asp Arg Ala Leu		
	290	295 300
Ser Ala His Arg Gly His Pro Gly Arg Leu Glu Glu Leu Val Thr Ala		
305	310	315 320
Leu Ala Thr Ala Ala Leu Arg Ala Ala Ala Lys Ala Leu Pro Gly Leu		
	325	330 335
Thr Pro Ser Gly Pro Val Val Arg Arg Arg Arg Ser Pro Val Leu Arg		
	340	345 350
Gly Thr Asn Arg Cys Pro Val Glu Leu		
	355	360

<210> 4
 <211> 1266
 <212> DNA
 <213> Saccharopolyspora erythraea

<220>
 <221> CDS
 <222> complement (4)..(1266)
 <223> /function= "involved in the biosynthesis of
 mycarose" /gene= "eryCIII" /note= "SEQ ID No 1
 from 1046 to 2308"

<400> 4
 tcatcgtggt tctctccttc ctgcggccag ttctcgcag atgccgacga cctcggccgg 60
 tgacggctcc gcgagcatgt cgtcgcgcgc cgcgcgccgc cggcgcggtt gggccgggtc 120
 gtcgaggacc cgcttcaccg actcccggag ctggtcgggg gtcagctcgg gcacgggcag 180
 cgcgatcccc gccccgaatt cctgcgtgcg ctgcgcgcgc acgccggtgt cccagccgctc 240
 gggcaggatc acctgcggca cgccgtggat cgccgcggtg tgccagctcc cgggtccgcc 300
 gtggtgcacc gtcgcgcgc aggtcggcag cagcgcgtgc atcgggacga agccgaccgt 360
 gcggacgttg tccgggatgt tcgcgacgcc ttctagctgc tgcgcgtcga aggtcgcgat 420

gatctcggcg tcgacgtcgc cgacggcacc cagcagctcc tcgatggaga cctgcccgat 480
gctgttctcg cggctggaga tcccagcgt gaggcacacg cggcggcgct cgggctcgtc 540
gtgcagccat tccggcacca cggacggccc gttgtagtcg acgtagcgca tcccagcggc 600
cttcaggccg gtgtcgagcc tgatcgcggc cggggcgggg tcgatcgctc actgcccgac 660
gaccacctcc tcgtcgaagg cggggccgcc gtacttctcc agcgtccagg tgagccactc 720
ggcgagcggg tcttcccggg gctcctccgg ctggtcgggc agcaggccga ggaagttctg 780
ccgcgcccgg gtggtgatgt cgggtcccca cagcagccgc gcgtgcggcg ttccggtcac 840
cgccgcccgc atgggcgcgg cgaaggtgag cggctcccag atgaccaggc cgggcccga 900
cttccggcag aacgagacca tgccttcgat gagcgtgtcc gggctcatca gggcgtagaa 960
ggtcgggggtg agcacggtct gcatgcccag caggtgctcc caggtcaagg tggcggggtc 1020
ccgctcgctg aagtccaggc tccggacgta gtcgatgatg tcgtggcccg cgtgggtcat 1080
gaagtccacg aggtcgacgt cggtgccgac cgggacggcg gtcagcccgg ccgcggtgat 1140
gtcctcggtg agcgcggggg acgcgaccac gcggacctcg tgccccgccg cgcggaacgc 1200
ccatgcgagg gggacgaggc cgaagaggtg gctcttgctg gccatggagg agaagacgac 1260
gcgcat 1266

<210> 5

<211> 421

<212> PRT

<213> Saccharopolyspora erythraea

<400> 5

Met Arg Val Val Phe Ser Ser Met Ala Ser Lys Ser His Leu Phe Gly
1 5 10 15
Leu Val Pro Leu Ala Trp Ala Phe Arg Ala Ala Gly His Glu Val Arg
20 25 30
Val Val Ala Ser Pro Ala Leu Thr Glu Asp Ile Thr Ala Ala Gly Leu
35 40 45
Thr Ala Val Pro Val Gly Thr Asp Val Asp Leu Val Asp Phe Met Thr
50 55 60
His Ala Gly His Asp Ile Ile Asp Tyr Val Arg Ser Leu Asp Phe Ser
65 70 75 80
Glu Arg Asp Pro Ala Thr Leu Thr Trp Glu His Leu Leu Gly Met Gln
85 90 95
Thr Val Leu Thr Pro Thr Phe Tyr Ala Leu Met Ser Pro Asp Thr Leu

100					105					110					
Ile	Glu	Gly	Met	Val	Ser	Phe	Cys	Arg	Lys	Trp	Arg	Pro	Asp	Leu	Val
	115						120					125			
Ile	Trp	Glu	Pro	Leu	Thr	Phe	Ala	Ala	Pro	Ile	Ala	Ala	Ala	Val	Thr
	130					135					140				
Gly	Thr	Pro	His	Ala	Arg	Leu	Leu	Trp	Gly	Pro	Asp	Ile	Thr	Thr	Arg
145					150					155					160
Ala	Arg	Gln	Asn	Phe	Leu	Gly	Leu	Leu	Pro	Asp	Gln	Pro	Glu	Glu	His
				165					170					175	
Arg	Glu	Asp	Pro	Leu	Ala	Glu	Trp	Leu	Thr	Trp	Thr	Leu	Glu	Lys	Tyr
			180					185					190		
Gly	Gly	Pro	Ala	Phe	Asp	Glu	Glu	Val	Val	Val	Gly	Gln	Trp	Thr	Ile
	195						200					205			
Asp	Pro	Ala	Pro	Ala	Ala	Ile	Arg	Leu	Asp	Thr	Gly	Leu	Lys	Thr	Val
	210					215					220				
Gly	Met	Arg	Tyr	Val	Asp	Tyr	Asn	Gly	Pro	Ser	Val	Val	Pro	Glu	Trp
225					230					235					240
Leu	His	Asp	Glu	Pro	Glu	Arg	Arg	Arg	Val	Cys	Leu	Thr	Leu	Gly	Ile
				245					250					255	
Ser	Ser	Arg	Glu	Asn	Ser	Ile	Gly	Gln	Val	Ser	Ile	Glu	Glu	Leu	Leu
			260					265					270		
Gly	Ala	Val	Gly	Asp	Val	Asp	Ala	Glu	Ile	Ile	Ala	Thr	Phe	Asp	Ala
	275						280					285			
Gln	Gln	Leu	Glu	Gly	Val	Ala	Asn	Ile	Pro	Asp	Asn	Val	Arg	Thr	Val
	290					295					300				
Gly	Phe	Val	Pro	Met	His	Ala	Leu	Leu	Pro	Thr	Cys	Ala	Ala	Thr	Val
305					310					315					320
His	His	Gly	Gly	Pro	Gly	Ser	Trp	His	Thr	Ala	Ala	Ile	His	Gly	Val
				325					330					335	
Pro	Gln	Val	Ile	Leu	Pro	Asp	Gly	Trp	Asp	Thr	Gly	Val	Arg	Ala	Gln
			340					345					350		
Arg	Thr	Gln	Glu	Phe	Gly	Ala	Gly	Ile	Ala	Leu	Pro	Val	Pro	Glu	Leu
	355						360					365			
Thr	Pro	Asp	Gln	Leu	Arg	Glu	Ser	Val	Lys	Arg	Val	Leu	Asp	Asp	Pro
	370					375					380				
Ala	His	Arg	Ala	Gly	Ala	Ala	Arg	Met	Arg	Asp	Asp	Met	Leu	Ala	Glu
385					390					395					400
Pro	Ser	Pro	Ala	Glu	Val	Val	Gly	Ile	Cys	Glu	Glu	Leu	Ala	Ala	Gly

405

410

415

Arg Arg Glu Pro Arg
420

<210> 6
<211> 8160
<212> DNA
<213> Saccharopolyspora erythraea

<220>
<221> CDS
<222> (242)..(1207)
<223> /function= "involved in the biosynthesis of
mycarose" /gene= "eryBIV" /transl_except= (pos:
242 .. 244, aa: Met)

<220>
<221> CDS
<222> (1210)..(2454)
<223> /function= "involved in the biosynthesis of
mycarose" /gene= "eryBV" /transl_except= (pos:
1210 .. 1212, aa: Met)

<220>
<221> CDS
<222> (2510)..(3220)
<223> /function= "involved in the biosynthesis of
desosamine" /gene= "eryCVI"

<220>
<221> CDS
<222> (3308)..(4837)
<223> /function= "involved in the biosynthesis of
mycarose" /gene= "eryBVI" /transl_except= (pos:
3308...3310, aa: Met)

<220>
<221> CDS
<222> (6080)..(7546)
<223> /function= "involved in the biosynthesis of
desosamine" /gene= "eryCV"

<220>
<221> CDS
<222> (7578)..(8156)
<223> /function= "involved in the biosynthesis of
mycarose" /gene= "eryBVII" /transl_except=
(pos:7578 .. 7580, aa: Met)

<220>
<221> mat_peptide
<222> (242)

<400> 6
tttgacaggt ccgccacgcg tccccctact cgacgaccac gcaatgggcg aacaatatag 60

gaaggatcaa gaggttgaca tcgcctcgtc gagccaacga acctgtgaac atctgcatgt 120
 tgacaagatc aacggcggct acctactgtg gtggcccagt gacgggttgc cgcacatcgc 180
 gctgggggaga ttctttgaat ttcgcccgtg gcaccgacct ggaaagcgag caaatgctcc 240
 g gtg aat ggg atc agt gat tcc ccg cgt caa ttg atc acc ctt ctg ggc 289
 Met Asn Gly Ile Ser Asp Ser Pro Arg Gln Leu Ile Thr Leu Leu Gly
 1 5 10 15
 gct tcc ggc ttc gtc ggg agc gcg gtt ctg cgc gag ctg cgc gac cac 337
 Ala Ser Gly Phe Val Gly Ser Ala Val Leu Arg Glu Leu Arg Asp His
 20 25 30
 ccg gtc cgg ctg cgc gcg gtg tcc cgc ggc gga gcg ccc gcg gtt ccg 385
 Pro Val Arg Leu Arg Ala Val Ser Arg Gly Gly Ala Pro Ala Val Pro
 35 40 45
 ccc ggc gcc gcg gag gtc gag gac ctg cgc gcc gac ctg ctg gaa ccg 433
 Pro Gly Ala Ala Glu Val Glu Asp Leu Arg Ala Asp Leu Leu Glu Pro
 50 55 60
 ggc cgg gcc gcc gcc gcg atc gag gac gcc gac gtg atc gtg cac ctg 481
 Gly Arg Ala Ala Ala Ala Ile Glu Asp Ala Asp Val Ile Val His Leu
 65 70 75 80
 gtg gcg cac gca gcg ggc ggt tcc acc tgg cgc agc gcc acc tcc gac 529
 Val Ala His Ala Ala Gly Gly Ser Thr Trp Arg Ser Ala Thr Ser Asp
 85 90 95
 ccg gaa gcc gag cgg gtc aac gtc ggc ctg atg cac gac ctc gtc ggc 577
 Pro Glu Ala Glu Arg Val Asn Val Gly Leu Met His Asp Leu Val Gly
 100 105 110
 gcg ctg cac gat cgc cgc agg tcg acg ccg ccc gtg ttg ctc tac gcg 625
 Ala Leu His Asp Arg Arg Arg Ser Thr Pro Pro Val Leu Leu Tyr Ala
 115 120 125
 agc acc gca cag gcc gcg aac ccg tcg gcg gcc agc agg tac gcg cag 673
 Ser Thr Ala Gln Ala Ala Asn Pro Ser Ala Ala Ser Arg Tyr Ala Gln
 130 135 140
 cag aag acc gag gcc gag cgc atc ctg cgc aaa gcc acc gac gag ggc 721
 Gln Lys Thr Glu Ala Glu Arg Ile Leu Arg Lys Ala Thr Asp Glu Gly
 145 150 155 160
 ccg gtg cgc ggc gtg atc ctg ccg ctg ccc gcc gtc tac ggc cag agc 769
 Arg Val Arg Gly Val Ile Leu Arg Leu Pro Ala Val Tyr Gly Gln Ser
 165 170 175
 ggc ccg tcc ggc ccc atg ggg ccg ggc gtg gtc gca gcg atg atc ccg 817
 Gly Pro Ser Gly Pro Met Gly Arg Gly Val Val Ala Ala Met Ile Arg
 180 185 190
 cgt gcc ctc gcc ggc gag ccg ctc acc atg tgg cac gac ggc ggc gtg 865
 Arg Ala Leu Ala Gly Glu Pro Leu Thr Met Trp His Asp Gly Gly Val

195	200	205	
cgc cgc gac ctg ctg cac gtc gag gac gtg gcc acc gcg ttc gcc gcc Arg Arg Asp Leu Leu His Val Glu Asp Val Ala Thr Ala Phe Ala Ala 210 215 220			913
gcg ctg gag cac cac gac gcg ctg gcc ggc ggc acg tgg gcg ctg ggc Ala Leu Glu His His Asp Ala Leu Ala Gly Gly Thr Trp Ala Leu Gly 225 230 235 240			961
gcc gac cga tcc gag ccg ctc ggc gac atc ttc cgg gcc gtc tcc ggc Ala Asp Arg Ser Glu Pro Leu Gly Asp Ile Phe Arg Ala Val Ser Gly 245 250 255			1009
agc gtc gcc cgg cag acc ggc agc ccc gcc gtc gac gtg gtc acc gtg Ser Val Ala Arg Gln Thr Gly Ser Pro Ala Val Asp Val Val Thr Val 260 265 270			1057
ccc gcg ccc gag cac gcc gag gcc aac gac ttc cgc agc gac gac atc Pro Ala Pro Glu His Ala Glu Ala Asn Asp Phe Arg Ser Asp Asp Ile 275 280 285			1105
gac tcc acc gag ttc cgc agc cgg acc ggc tgg cgc ccc cgg gtt tcc Asp Ser Thr Glu Phe Arg Ser Arg Thr Gly Trp Arg Pro Arg Val Ser 290 295 300			1153
ctc acc gac ggc atc gac cgg acg gtg gcc gcc ctg acc ccc acc gag Leu Thr Asp Gly Ile Asp Arg Thr Val Ala Ala Leu Thr Pro Thr Glu 305 310 315 320			1201
gag cac ta gtg cgg gta ctg ctg acg tcc ttc gcg cac cgc acg cac Glu His Met Arg Val Leu Leu Thr Ser Phe Ala His Arg Thr His 325 330 335			1248
ttc cag gga ctg gtc ccg ctg gcg tgg gcg ctg cgc acc gcg ggt cac Phe Gln Gly Leu Val Pro Leu Ala Trp Ala Leu Arg Thr Ala Gly His 340 345 350			1296
gac gtg cgc gtg gcc gcc cag ccc gcg ctc acc gac gcg gtc atc ggc Asp Val Arg Val Ala Ala Gln Pro Ala Leu Thr Asp Ala Val Ile Gly 355 360 365			1344
gcc ggt ctc acc gcg gta ccc gtc ggc tcc gac cac cgg ctg ttc gac Ala Gly Leu Thr Ala Val Pro Val Gly Ser Asp His Arg Leu Phe Asp 370 375 380			1392
atc gtc ccg gaa gtc gcc gct cag gtg cac cgc tac tcc ttc tac ctg Ile Val Pro Glu Val Ala Ala Gln Val His Arg Tyr Ser Phe Tyr Leu 385 390 395			1440
gac ttc tac cac cgc gag cag gag ctg cac tcg tgg gag ttc ctg ctc Asp Phe Tyr His Arg Glu Gln Glu Leu His Ser Trp Glu Phe Leu Leu 400 405 410 415			1488
ggc atg cag gag gcc acc tcg cgg tgg gta tac ccg gtg gtc aac aac Gly Met Gln Glu Ala Thr Ser Arg Trp Val Tyr Pro Val Val Asn Asn			1536

420										425					430					
gac tcc ttc gtc gcc gag ctg gtc gac ttc gcc cgg gac tgg cgt cct	1584																			
Asp Ser Phe Val Ala Glu Leu Val Asp Phe Ala Arg Asp Trp Arg Pro																				
435 440 445																				
gac ctg gtg ctc tgg gag ccg ttc acc ttc gcc ggc gcc gtc gcg gcc	1632																			
Asp Leu Val Leu Trp Glu Pro Phe Thr Phe Ala Gly Ala Val Ala Ala																				
450 455 460																				
cgg gcc tgc gga gcc gcg cac gcc cgg ctg ctg tgg ggc agc gac ctc	1680																			
Arg Ala Cys Gly Ala Ala His Ala Arg Leu Leu Trp Gly Ser Asp Leu																				
465 470 475																				
acc ggc tac ttc cgc ggc ccg ttc cag gcg caa cgc ctg cga cgg ccg	1728																			
Thr Gly Tyr Phe Arg Gly Arg Phe Gln Ala Gln Arg Leu Arg Arg Pro																				
480 485 490 495																				
ccg gag gac cgg ccg gac ccg ctg ggc acg tgg ctg acc gag gtc gcg	1776																			
Pro Glu Asp Arg Pro Asp Pro Leu Gly Thr Trp Leu Thr Glu Val Ala																				
500 505 510																				
ggg cgc ttc ggc gtc gaa ttc ggc gag gac ctc gcg gtc ggg cag tgg	1824																			
Gly Arg Phe Gly Val Glu Phe Gly Glu Asp Leu Ala Val Gly Gln Trp																				
515 520 525																				
tcg gtc gac cag ttg ccg ccg agt ttc cgg ctg gac acc gga atg gaa	1872																			
Ser Val Asp Gln Leu Pro Pro Ser Phe Arg Leu Asp Thr Gly Met Glu																				
530 535 540																				
acc gtt gtc gcg ccg acc ctg ccc tac aac ggc gcg tcg gtg gtt ccg	1920																			
Thr Val Val Ala Arg Thr Leu Pro Tyr Asn Gly Ala Ser Val Val Pro																				
545 550 555																				
gac tgg ctc aag aag ggc agt gcg act cga cgc atc tgc att acc gga	1968																			
Asp Trp Leu Lys Lys Gly Ser Ala Thr Arg Arg Ile Cys Ile Thr Gly																				
560 565 570 575																				
ggg ttc tcc gga ctc ggg ctc gcc gcc gat gcc gat cag ttc gcg ccg	2016																			
Gly Phe Ser Gly Leu Gly Leu Ala Ala Asp Ala Asp Gln Phe Ala Arg																				
580 585 590																				
acg ctc gcg cag ctc gcg cga ttc gat ggc gaa atc gtg gtt acg ggt	2064																			
Thr Leu Ala Gln Leu Ala Arg Phe Asp Gly Glu Ile Val Val Thr Gly																				
595 600 605																				
tcc ggt ccg gat acc tcc gcg gta ccg gac aac att cgt ttg gtg gat	2112																			
Ser Gly Pro Asp Thr Ser Ala Val Pro Asp Asn Ile Arg Leu Val Asp																				
610 615 620																				
ttc gtt ccg atg ggc gtt ctg ctc cag aac tgc gcg gcg atc atc cac	2160																			
Phe Val Pro Met Gly Val Leu Leu Gln Asn Cys Ala Ala Ile Ile His																				
625 630 635																				
cac ggc ggg gcc gga acc tgg gcc acg gca ctg cac cac gga att ccg	2208																			
His Gly Gly Ala Gly Thr Trp Ala Thr Ala Leu His His Gly Ile Pro																				
640 645 650 655																				

caa ata tca gtt gca cat gaa tgg gat tgc atg cta cgc ggc cag cag	2256
Gln Ile Ser Val Ala His Glu Trp Asp Cys Met Leu Arg Gly Gln Gln	
660 665 670	
acc gcg gaa ctg ggc gcg gga atc tac ctc cgg ccg gac gag gtc gat	2304
Thr Ala Glu Leu Gly Ala Gly Ile Tyr Leu Arg Pro Asp Glu Val Asp	
675 680 685	
gcc gac tca ttg gcg agc gcc ctc acc cag gtg gtc gag gac ccc acc	2352
Ala Asp Ser Leu Ala Ser Ala Leu Thr Gln Val Val Glu Asp Pro Thr	
690 695 700	
tac acc gag aac gcg gtg aag ctt cgc gag gag gcg ctg tcc gac ccg	2400
Tyr Thr Glu Asn Ala Val Lys Leu Arg Glu Glu Ala Leu Ser Asp Pro	
705 710 715	
acg ccg cag gag atc gtc ccg cga ctg gag gaa ctc acg cgc cgc cac	2448
Thr Pro Gln Glu Ile Val Pro Arg Leu Glu Glu Leu Thr Arg Arg His	
720 725 730 735	
gcc ggc tagcgggtttc cgaccgacaa gtccgtccga cagcacacct ccggagggag	2504
Ala Gly	
caggg atg tac gag ggc ggg ttc gcc gag ctt tac gac cgg ttc tac cgc	2554
Met Tyr Glu Gly Gly Phe Ala Glu Leu Tyr Asp Arg Phe Tyr Arg	
740 745 750	
ggc ccg gcc aag gac tac gcg gcc gag gcc gcg cag gtc gcg ccg ctg	2602
Gly Arg Gly Lys Asp Tyr Ala Ala Glu Ala Ala Gln Val Ala Arg Leu	
755 760 765	
gtc aga gac cgc ctg ccc tcg gct tcc tcg ctg ctc gac gtg gcc tgc	2650
Val Arg Asp Arg Leu Pro Ser Ala Ser Ser Leu Leu Asp Val Ala Cys	
770 775 780	
ggg acc gcc acc cac ctg cgc ccg ttc gcc gac ctc ttc gac gac gtg	2698
Gly Thr Gly Thr His Leu Arg Arg Phe Ala Asp Leu Phe Asp Asp Val	
785 790 795 800	
acc ggg ctg gag ctg tcg gcg gcg atg atc gag gtc gcc ccg ccg cag	2746
Thr Gly Leu Glu Leu Ser Ala Ala Met Ile Glu Val Ala Arg Pro Gln	
805 810 815	
ctc gcc gcc atc ccg gtg ctg cag ggc gac atg cgc gac ttc gcg ctg	2794
Leu Gly Gly Ile Pro Val Leu Gln Gly Asp Met Arg Asp Phe Ala Leu	
820 825 830	
gat cgc gag ttc gac gcc gtc acc tgc atg ttc agc tcc atc ggg cac	2842
Asp Arg Glu Phe Asp Ala Val Thr Cys Met Phe Ser Ser Ile Gly His	
835 840 845	
atg cgc gac gcc gcc gag ctg gac cag gcg ctg gcg tcc ttc gcc cgc	2890
Met Arg Asp Gly Ala Glu Leu Asp Gln Ala Leu Ala Ser Phe Ala Arg	
850 855 860	
cac ctc gcc ccc gcc gcc gtc gtg gtg gtc gaa ccg tgg tgg ttc ccg	2938

His 865	Leu	Ala	Pro	Gly	Gly 870	Val	Val	Val	Val	Glu 875	Pro	Trp	Trp	Phe	Pro 880	
gag Glu	gac Asp	ttc Phe	ctc Leu	gac Asp 885	ggc Gly	tac Tyr	gtg Val	gcc Ala	ggg Gly 890	gac Asp	gtg Val	gtg Val	cgc Arg	gac Asp 895	ggc Gly	2986
gac Asp	ctg Leu	acg Thr	atc Ile 900	tcg Ser	cgc Arg	gtc Val	tcg Ser	cac His 905	tcc Ser	gtg Val	cgc Arg	gcc Ala	ggc Gly 910	ggc Gly	gcg Ala	3034
acc Thr	cgg Arg	atg Met 915	gag Glu	atc Ile	cac His	tgg Trp	gtc Val	gtg Val	gcc Ala	gac Asp	cgc Ala	gtg Val	aac Asn 925	ggg Gly	ccg Pro	3082
cgg Arg	cac His 930	cac His	gtg Val	gag Glu	cac His	tac Tyr 935	gag Glu	atc Ile	acg Thr	ctc Leu	ttc Phe 940	gag Glu	cgg Arg	cag Gln	cag Gln	3130
tac Tyr 945	gag Glu	aag Lys	gcc Ala	ttc Phe	acc Thr 950	gcg Ala	gcc Ala	ggg Gly	tgc Cys	gct Ala	gtg Val	cag Gln	tac Tyr	ctg Leu	gag Glu 960	3178
ggc Gly	gga Gly	ccc Pro	tcc Ser	gga Gly 965	cgc Arg	ggg Gly	ttg Leu	ttc Phe	gtc Val 970	ggg Gly	gtg Val	cgc Arg	gga Gly			3220
tgacccgtgc gttcgcgttt tccgttccctg gcacaggtga tccgctccac gggccctttc																3280
cccgcctga cccgaccctt acagtga gtg cgg gtc ttg atc gac aac gcc cgg Met Arg Val Leu Ile Asp Asn Ala Arg 975 980																3334
cgg Arg	cag Gln 985	caa Gln	gcg Ala	gag Glu	ccg Pro	tcg Ser 990	acg Thr	aca Thr	ccg Pro	cag Gln	gga Gly 995	gag Glu	tcg Ser	atg Met	ggg Gly	3382
gat Asp 1000	cgg Arg	acc Thr	ggc Gly	gac Asp	cgg Arg	acg Thr	att Ile	ccg Pro	gaa Glu	tcc Ser	tcg Ser	cag Gln	acc Thr	gca Ala	acg Thr 1015	3430
cgt Arg	ttc Phe	ctg Leu	ctc Leu	ggc Gly 1020	gac Asp	ggc Gly	gga Gly	atc Ile	ccc Pro	acc Thr	gcc Ala	acg Thr	gcg Ala	gaa Glu 1030	acc Thr	3478
cac His	gac Asp	tgg Trp	ctg Leu	acc Thr	cgc Arg	aac Asn	ggc Gly	gcc Ala	gag Glu	cag Gln	cgg Arg	ctc Leu	gag Glu	gtg Val	gcg Ala	3526
cgc Arg	gtg Val	ccg Pro	ttc Phe	agc Ser	gcc Ala	atg Met	gac Asp	cgc Arg	tgg Trp	tcg Ser	ttc Phe	cag Gln	ccc Pro	gag Glu	gac Asp	3574
ggc Gly 1065	agg Arg	ctc Leu	gcc Ala	cac His	gag Glu	tcc Ser	ggg Gly	cgc Arg	ttc Phe	ttc Phe	tcc Ser	atc Ile	gag Glu	ggc Gly	ctg Leu	3622

cac gtg cgg acg aac ttc ggc tgg cgg cgg gac tgg atc cag ccc atc	3670
His Val Arg Thr Asn Phe Gly Trp Arg Arg Asp Trp Ile Gln Pro Ile	
1080 1085 1090 1095	
atc gtg cag ccc gag atc ggc ttc ctc ggc ctc atc gtc aag gag ttc	3718
Ile Val Gln Pro Glu Ile Gly Phe Leu Gly Leu Ile Val Lys Glu Phe	
1100 1105 1110	
gac ggt gtg ctg cac gtg ctg gcg cag gcc aag gcc gag ccg ggc aac	3766
Asp Gly Val Leu His Val Leu Ala Gln Ala Lys Ala Glu Pro Gly Asn	
1115 1120 1125	
atc aac gcc gtc cag ctc tcc ccg acc ctg cag gcg acc cgc agc aac	3814
Ile Asn Ala Val Gln Leu Ser Pro Thr Leu Gln Ala Thr Arg Ser Asn	
1130 1135 1140	
tac acc ggc gtc cac cgc ggc tcg aag gtc cgg ttc atc gag tac ttc	3862
Tyr Thr Gly Val His Arg Gly Ser Lys Val Arg Phe Ile Glu Tyr Phe	
1145 1150 1155	
aac ggc acg cgc ccg agc cgg atc ctc gtc gac gtg ctc cag tcc gag	3910
Asn Gly Thr Arg Pro Ser Arg Ile Leu Val Asp Val Leu Gln Ser Glu	
1160 1165 1170 1175	
cag ggc gcg tgg ttc ctg cgc aag cgc aac cgg aac atg gtc gtc gag	3958
Gln Gly Ala Trp Phe Leu Arg Lys Arg Asn Arg Asn Met Val Val Glu	
1180 1185 1190	
gtg ttc gac gac ctg ccc gag cac ccg aac ttc cgg tgg ctg acc gtc	4006
Val Phe Asp Asp Leu Pro Glu His Pro Asn Phe Arg Trp Leu Thr Val	
1195 1200 1205	
gcg cag ctg cgg gcg atg ctg cac cac gac aac gtg gtg aac atg gac	4054
Ala Gln Leu Arg Ala Met Leu His His Asp Asn Val Val Asn Met Asp	
1210 1215 1220	
ctg cgc acc gtg ctg gcc tgc gtc ccg acc gcc gtg gag cgg gac cgg	4102
Leu Arg Thr Val Leu Ala Cys Val Pro Thr Ala Val Glu Arg Asp Arg	
1225 1230 1235	
gcc gac gac gtg ctc gcg cgc ctg ccc gag ggc tcg ttc cag gcc cgg	4150
Ala Asp Asp Val Leu Ala Arg Leu Pro Glu Gly Ser Phe Gln Ala Arg	
1240 1245 1250 1255	
ctg ctg cac tcg ttc atc ggc gcg ggc acc ccg gcc aac aac atg aac	4198
Leu Leu His Ser Phe Ile Gly Ala Gly Thr Pro Ala Asn Asn Met Asn	
1260 1265 1270	
agc ctg ctg agc tgg atc tcc gac gtg cgc gcc agg cgc gag ttc gtg	4246
Ser Leu Leu Ser Trp Ile Ser Asp Val Arg Ala Arg Arg Glu Phe Val	
1275 1280 1285	
cag cgc ggc cgc ccg ctg ccc gac atc gag cgc agc ggg tgg atc cgc	4294
Gln Arg Gly Arg Pro Leu Pro Asp Ile Glu Arg Ser Gly Trp Ile Arg	
1290 1295 1300	
cgc gac gac ggc atc gag cac gag gag aag aag tac ttc gac gtc ttc	4342

Arg Asp Asp Gly Ile Glu His Glu Glu Lys Lys Tyr Phe Asp Val Phe
 1305 1310 1315
 ggc gtc acg gtg gcg acc agc gac cgc gag gtc aac tcg tgg atg cag 4390
 Gly Val Thr Val Ala Thr Ser Asp Arg Glu Val Asn Ser Trp Met Gln
 1320 1325 1330 1335
 ccg ctg ctc tcg ccc gcc aac aac ggc ctg ctc gcc ctg ctg gtc aag 4438
 Pro Leu Leu Ser Pro Ala Asn Asn Gly Leu Leu Ala Leu Leu Val Lys
 1340 1345 1350
 gac atc ggc ggc acg ttg cac gcg ctc gtg cag ctg cgc acc gag gcg 4486
 Asp Ile Gly Gly Thr Leu His Ala Leu Val Gln Leu Arg Thr Glu Ala
 1355 1360 1365
 ggc ggg atg gac gtc gcc gag ctg gcg cct acg gtg cac tgc cag ccc 4534
 Gly Gly Met Asp Val Ala Glu Leu Ala Pro Thr Val His Cys Gln Pro
 1370 1375 1380
 gac aac tac gcc gac gcg ccc gag gag ttc cga ccg gcc tat gtg gac 4582
 Asp Asn Tyr Ala Asp Ala Pro Glu Glu Phe Arg Pro Ala Tyr Val Asp
 1385 1390 1395
 tac gtg ttg aac gtg ccg cgc tcg cag gtc cgc tac gac gca tgg cac 4630
 Tyr Val Leu Asn Val Pro Arg Ser Gln Val Arg Tyr Asp Ala Trp His
 1400 1405 1410 1415
 tcc gag gag ggc ggc cgg ttc tac cgc aac gag aac cgg tac atg ctg 4678
 Ser Glu Glu Gly Gly Arg Phe Tyr Arg Asn Glu Asn Arg Tyr Met Leu
 1420 1425 1430
 atc gag gtg ccc gcc gac ttc gac gcc agt gcc gct ccc gac cac cgg 4726
 Ile Glu Val Pro Ala Asp Phe Asp Ala Ser Ala Ala Pro Asp His Arg
 1435 1440 1445
 tgg atg acc ttc gac cag atc acc tac ctg ctc ggg cac agc cac tac 4774
 Trp Met Thr Phe Asp Gln Ile Thr Tyr Leu Leu Gly His Ser His Tyr
 1450 1455 1460
 gtc aac atc cag ctg cgc agc atc atc gcg tgc gcc tcg gcc gtc tac 4822
 Val Asn Ile Gln Leu Arg Ser Ile Ile Ala Cys Ala Ser Ala Val Tyr
 1465 1470 1475
 acc agg acc gcc gga tgaaacgcgc gctgaccgac ctggcgatct tcggcgggccc 4877
 Thr Arg Thr Ala Gly
 1480
 cgaggcattc ctgcacaccc tctacgtggg caggccgacc gtcgggggacc gggagcggtt 4937
 cttcgcccgc ctggagtggg cgctgaacaa caactggctg accaacggcg gaccactggt 4997
 gcgcgagttc gagggccggg tcgccgacct ggcgggtgtc cgccactgcg tggccacctg 5057
 caacgcgacg gtcgcgctgc aactggtgct gcgcgcgagc gacgtgtccg gcgaggtcgt 5117
 catgccttcg atgacgttcg cggccaccgc gcacgcggcg agctggctgg ggctggaacc 5177

ggtgttctgc gacgtggacc ccgagaccgg cctgctcgac cccgagcacg tcgctcgct 5237
 ggtgacaccg cggacgggcg cgatcatcgg cgtgcacctg tggggcaggc ccgctccggt 5297
 cgaggcgctg gagaagatcg ccgccgagca ccagggtcaaa ctcttcttcg acgccgcgca 5357
 cgcgctgggc tgcaccgccg gcggggcgcc ggtcggcgcc ttcggcaacg ccgaggtggt 5417
 cagcttccac gccacgaagg cggtcacctc gttcgagggc ggccgcatcg tcaccgacga 5477
 cgggctgctg gccgaccgca tccgcgccat gcacaacttc gggatcgac ccgacaagct 5537
 ggtgaccgat gtcggcacca acggcaagat gagcgagtgc gccgcggcga tgggcctcac 5597
 ctcgctcgac gccttcgccg agaccagggt gcacaaccgc ctcaaccacg cgctctactc 5657
 cgacgagctc cgcgacgtgc gcggcatatc cgtgcacgcg ttcgatcctg gcgagcagaa 5717
 caactaccag tacgtgatca tctcggtgga ctccgcggcc accggcatcg accgcgacca 5777
 gttgcaggcg atcctgcgag cggagaaggt tgtggcacia ccctacttct ccccggggtg 5837
 ccaccagatg cagccgtacc ggaccgagcc gccgctgcgg ctggagaaca ccgaacagct 5897
 ctccgaccgg gtgctcgcg tgcccaccgg ccccgcggtg tccagcgagg acatccggcg 5957
 ggtgtgcgac atcatccggc tcgccgccac cagcggcgag ctgatcaacg cgcaatggga 6017
 ccagaggacg cgcaacgggt cgtgacgacc tgcgccacia gtgccaggag gttcgtctcc 6077
 cg atg aac aca act cgt acg gca acc gcc cag gaa gcg ggg gtc gcc 6124
 Met Asn Thr Thr Arg Thr Ala Thr Ala Gln Glu Ala Gly Val Ala
 1485 1490 1495
 gac gcg gcg cgc ccg gac gtc gac cgg cgg gcg gtc gtg cgg gcg ctg 6172
 Asp Ala Ala Arg Pro Asp Val Asp Arg Arg Ala Val Val Arg Ala Leu
 1500 1505 1510 1515
 agc tcg gag gtc tcc cgc gtc acc ggc gcc ggt gac ggt gac gcc gac 6220
 Ser Ser Glu Val Ser Arg Val Thr Gly Ala Gly Asp Gly Asp Ala Asp
 1520 1525 1530
 gtg cag gcc gcc cgg ctc gcc gac ctc gcc gcg cac tac ggg gcg cac 6268
 Val Gln Ala Ala Arg Leu Ala Asp Leu Ala Ala His Tyr Gly Ala His
 1535 1540 1545
 ccg ttc acg ccg ctg gag cag acg cgt gcg cgg ctc ggc ctg gac cgc 6316
 Pro Phe Thr Pro Leu Glu Gln Thr Arg Ala Arg Leu Gly Leu Asp Arg
 1550 1555 1560
 gcg gag ttc gcc cac ctg ctc gac ctg ttc ggc cgc atc ccg gac ctg 6364
 Ala Glu Phe Ala His Leu Leu Asp Leu Phe Gly Arg Ile Pro Asp Leu
 1565 1570 1575
 ggc acc gcg gtg gag cac ggt ccg gcg ggc aag tac tgg tcc aac acg 6412
 Gly Thr Ala Val Glu His Gly Pro Ala Gly Lys Tyr Trp Ser Asn Thr
 1580 1585 1590 1595

atc aag ccg ctg gac gcc gca ggc gca ctg gac gcg gcg gtc tac cgc Ile Lys Pro Leu Asp Ala Ala Gly Ala Leu Asp Ala Ala Val Tyr Arg 1600 1605 1610	6460
aag cct gcc ttc ccc tac agc gtc ggc ctg tac ccc ggg ccg acg tgc Lys Pro Ala Phe Pro Tyr Ser Val Gly Leu Tyr Pro Gly Pro Thr Cys 1615 1620 1625	6508
atg ttc cgc tgc cac ttc tgc gtg cgg gtg acc ggt gcc cgc tac gag Met Phe Arg Cys His Phe Cys Val Arg Val Thr Gly Ala Arg Tyr Glu 1630 1635 1640	6556
gcc gca tcg gtc ccg gcg ggc aac gag acg ctg gcc gcg atc atc gac Ala Ala Ser Val Pro Ala Gly Asn Glu Thr Leu Ala Ala Ile Ile Asp 1645 1650 1655	6604
gag gtg ccc acg gac aac ccg aag gcg atg tac atg tcg ggc ggg ctc Glu Val Pro Thr Asp Asn Pro Lys Ala Met Tyr Met Ser Gly Gly Leu 1660 1665 1670 1675	6652
gag ccg ctg acc aac ccc ggt ctc ggc gag ctg gtg tcg cac gcc gcc Glu Pro Leu Thr Asn Pro Gly Leu Gly Glu Leu Val Ser His Ala Ala 1680 1685 1690	6700
ggg cgc ggt ttc gac ctc acc gtc tac acc aac gcc ttc gcc ctc acc Gly Arg Gly Phe Asp Leu Thr Val Tyr Thr Asn Ala Phe Ala Leu Thr 1695 1700 1705	6748
gag cag acg ctg aac cgc cag ccc ggc ctg tgg gag ctg ggc gcg atc Glu Gln Thr Leu Asn Arg Gln Pro Gly Leu Trp Glu Leu Gly Ala Ile 1710 1715 1720	6796
cgc acg tcc ctc tac ggg ctg aac aac gac gag tac gag acg acc acc Arg Thr Ser Leu Tyr Gly Leu Asn Asn Asp Glu Tyr Glu Thr Thr Thr 1725 1730 1735	6844
ggc aag cgc ggc gct ttc gaa cgc gtc aag aag aac ctg cag ggc ttc Gly Lys Arg Gly Ala Phe Glu Arg Val Lys Lys Asn Leu Gln Gly Phe 1740 1745 1750 1755	6892
ctg cgg atg cgc gcc gag cgg gac gcg ccg atc cgg ctc ggc ttc aac Leu Arg Met Arg Ala Glu Arg Asp Ala Pro Ile Arg Leu Gly Phe Asn 1760 1765 1770	6940
cac atc atc ctg ccg gga cgg gcc gac cgg ctc acc gac ctc gtc gac His Ile Ile Leu Pro Gly Arg Ala Asp Arg Leu Thr Asp Leu Val Asp 1775 1780 1785	6988
ttc atc gcc gag ctc aac gag tcc agc ccg caa cgg ccg ctg gac ttc Phe Ile Ala Glu Leu Asn Glu Ser Ser Pro Gln Arg Pro Leu Asp Phe 1790 1795 1800	7036
gtg acg gtg cgc gag gac tac agc ggc cgc gac gac ggc cgg ctg tcg Val Thr Val Arg Glu Asp Tyr Ser Gly Arg Asp Asp Gly Arg Leu Ser 1805 1810 1815	7084

gac tcc gag cgc aac gag ctg cgc gag ggc ctg gtg cgg ttc gtc gac Asp Ser Glu Arg Asn Glu Leu Arg Glu Gly Leu Val Arg Phe Val Asp 1820 1825 1830 1835	7132
tac gcc gcc gag cgg acc ccg ggc atg cac atc gac ctg ggc tac gcc Tyr Ala Ala Glu Arg Thr Pro Gly Met His Ile Asp Leu Gly Tyr Ala 1840 1845 1850	7180
ctg gag agc ctg cgg cgg ggt gtg gac gcc gag ctg ctg cgc atc cgg Leu Glu Ser Leu Arg Arg Gly Val Asp Ala Glu Leu Leu Arg Ile Arg 1855 1860 1865	7228
ccg gag acg atg cgt ccc acc gcg cac ccc cag gtc gcg gtg cag atc Pro Glu Thr Met Arg Pro Thr Ala His Pro Gln Val Ala Val Gln Ile 1870 1875 1880	7276
gac ctg ctc ggc gac gtc tac ctc tac cgc gag gcg ggc ttc ccg gag Asp Leu Leu Gly Asp Val Tyr Leu Tyr Arg Glu Ala Gly Phe Pro Glu 1885 1890 1895	7324
ctg gag ggc gcc acc cgc tac atc gcg ggc cgg gtc acc ccg tcg acc Leu Glu Gly Ala Thr Arg Tyr Ile Ala Gly Arg Val Thr Pro Ser Thr 1900 1905 1910 1915	7372
agc ctg cgc gag gtg gtg gag aac ttc gtg ctg gag aac gag ggc gtg Ser Leu Arg Glu Val Val Glu Asn Phe Val Leu Glu Asn Glu Gly Val 1920 1925 1930	7420
cag ccc cgc ccc ggc gac gag tac ttc ctc gac ggc ttc gac cag tcg Gln Pro Arg Pro Gly Asp Glu Tyr Phe Leu Asp Gly Phe Asp Gln Ser 1935 1940 1945	7468
gtg acc gca cgg ctc aac cag ctc gaa cga gac atc gcc gac ggg tgg Val Thr Ala Arg Leu Asn Gln Leu Glu Arg Asp Ile Ala Asp Gly Trp 1950 1955 1960	7516
gag gac cac cgc ggc ttc ctg cgc gga agg tgaaccggag ttgcgagtac Glu Asp His Arg Gly Phe Leu Arg Gly Arg 1965 1970	7566
gtgagctggc g gtg gcg ggc ggt ttc gag ttc acc ccc gac ccg aag cag Met Ala Gly Gly Phe Glu Phe Thr Pro Asp Pro Lys Gln 1975 1980 1985	7616
gac cgg cgg ggc ctg ttc gtg tct ccg ctg cag gac gag gcg ttc gtg Asp Arg Arg Gly Leu Phe Val Ser Pro Leu Gln Asp Glu Ala Phe Val 1990 1995 2000	7664
ggc gcg gtg ggc cat cgg ttc ccc gtc gcc cag atg aac cac atc gtc Gly Ala Val Gly His Arg Phe Pro Val Ala Gln Met Asn His Ile Val 2005 2010 2015	7712
tcc gcc cgg ggc gtg ctg cgc ggg ctg cac ttc acc acc acc ccg ccg Ser Ala Arg Gly Val Leu Arg Gly Leu His Phe Thr Thr Thr Pro Pro 2020 2025 2030	7760
ggg cag tgc aag tac gtc tac tgc gcg cgc ggc cgg gcg ctc gac gtc	7808

Gly Gln Cys Lys Tyr Val Tyr Cys Ala Arg Gly Arg Ala Leu Asp Val
 2035 2040 2045 2050

atc gtc gac atc cgg gtc ggc tcg ccg acg ttc ggg aag tgg gac gcg 7856
 Ile Val Asp Ile Arg Val Gly Ser Pro Thr Phe Gly Lys Trp Asp Ala
 2055 2060 2065

gtg gag atg gac acc gag cac ttc cgg gcg gtc tac ttc ccc agg ggc 7904
 Val Glu Met Asp Thr Glu His Phe Arg Ala Val Tyr Phe Pro Arg Gly
 2070 2075 2080

acc gcg cac gcc ttc ctc gcg ctt gag gac gac acc ctg atg tcg tac 7952
 Thr Ala His Ala Phe Leu Ala Leu Glu Asp Asp Thr Leu Met Ser Tyr
 2085 2090 2095

ctg gtc agc acg ccg tac gtg gcc gag tac gag cag gcg atc gac ccg 8000
 Leu Val Ser Thr Pro Tyr Val Ala Glu Tyr Glu Gln Ala Ile Asp Pro
 2100 2105 2110

ttc gac ccc gcg ctg ggt ctg ccg tgg ccc gcg gac ctg gag gtc gtg 8048
 Phe Asp Pro Ala Leu Gly Leu Pro Trp Pro Ala Asp Leu Glu Val Val
 2115 2120 2125 2130

ctc tcc gac cgc gac acg gtg gcc gtg gac ctg gag acc gcc agg cgg 8096
 Leu Ser Asp Arg Asp Thr Val Ala Val Asp Leu Glu Thr Ala Arg Arg
 2135 2140 2145

cga ggg atg ctg ccc gac tac gcc gac tgc ctc ggc gag gag ccc gcc 8144
 Arg Gly Met Leu Pro Asp Tyr Ala Asp Cys Leu Gly Glu Glu Pro Ala
 2150 2155 2160

agc acc ggc agg tgac 8160
 Ser Thr Gly Arg
 2165

<210> 7
 <211> 322
 <212> PRT
 <213> Saccharopolyspora erythraea

<400> 7
 Met Asn Gly Ile Ser Asp Ser Pro Arg Gln Leu Ile Thr Leu Leu Gly
 1 5 10 15
 Ala Ser Gly Phe Val Gly Ser Ala Val Leu Arg Glu Leu Arg Asp His
 20 25 30
 Pro Val Arg Leu Arg Ala Val Ser Arg Gly Gly Ala Pro Ala Val Pro
 35 40 45
 Pro Gly Ala Ala Glu Val Glu Asp Leu Arg Ala Asp Leu Leu Glu Pro
 50 55 60
 Gly Arg Ala Ala Ala Ala Ile Glu Asp Ala Asp Val Ile Val His Leu
 65 70 75 80

Leu Val Pro Leu Ala Trp Ala Leu Arg Thr Ala Gly His Asp Val Arg
 20 25 30

Val Ala Ala Gln Pro Ala Leu Thr Asp Ala Val Ile Gly Ala Gly Leu
 35 40 45

Thr Ala Val Pro Val Gly Ser Asp His Arg Leu Phe Asp Ile Val Pro
 50 55 60

Glu Val Ala Ala Gln Val His Arg Tyr Ser Phe Tyr Leu Asp Phe Tyr
 65 70 75 80

His Arg Glu Gln Glu Leu His Ser Trp Glu Phe Leu Leu Gly Met Gln
 85 90 95

Glu Ala Thr Ser Arg Trp Val Tyr Pro Val Val Asn Asn Asp Ser Phe
 100 105 110

Val Ala Glu Leu Val Asp Phe Ala Arg Asp Trp Arg Pro Asp Leu Val
 115 120 125

Leu Trp Glu Pro Phe Thr Phe Ala Gly Ala Val Ala Ala Arg Ala Cys
 130 135 140

Gly Ala Ala His Ala Arg Leu Leu Trp Gly Ser Asp Leu Thr Gly Tyr
 145 150 155 160

Phe Arg Gly Arg Phe Gln Ala Gln Arg Leu Arg Arg Pro Pro Glu Asp
 165 170 175

Arg Pro Asp Pro Leu Gly Thr Trp Leu Thr Glu Val Ala Gly Arg Phe
 180 185 190

Gly Val Glu Phe Gly Glu Asp Leu Ala Val Gly Gln Trp Ser Val Asp
 195 200 205

Gln Leu Pro Pro Ser Phe Arg Leu Asp Thr Gly Met Glu Thr Val Val
 210 215 220

Ala Arg Thr Leu Pro Tyr Asn Gly Ala Ser Val Val Pro Asp Trp Leu
 225 230 235 240

Lys Lys Gly Ser Ala Thr Arg Arg Ile Cys Ile Thr Gly Gly Phe Ser
 245 250 255

Gly Leu Gly Leu Ala Ala Asp Ala Asp Gln Phe Ala Arg Thr Leu Ala
 260 265 270

Gln Leu Ala Arg Phe Asp Gly Glu Ile Val Val Thr Gly Ser Gly Pro
 275 280 285

Asp Thr Ser Ala Val Pro Asp Asn Ile Arg Leu Val Asp Phe Val Pro
 290 295 300

Met Gly Val Leu Leu Gln Asn Cys Ala Ala Ile Ile His His Gly Gly
 305 310 315 320

Ala Gly Thr Trp Ala Thr Ala Leu His His Gly Ile Pro Gln Ile Ser
325 330 335

Val Ala His Glu Trp Asp Cys Met Leu Arg Gly Gln Gln Thr Ala Glu
340 345 350

Leu Gly Ala Gly Ile Tyr Leu Arg Pro Asp Glu Val Asp Ala Asp Ser
355 360 365

Leu Ala Ser Ala Leu Thr Gln Val Val Glu Asp Pro Thr Tyr Thr Glu
370 375 380

Asn Ala Val Lys Leu Arg Glu Glu Ala Leu Ser Asp Pro Thr Pro Gln
385 390 395 400

Glu Ile Val Pro Arg Leu Glu Glu Leu Thr Arg Arg His Ala Gly
405 410 415

<210> 9

<211> 237

<212> PRT

<213> Saccharopolyspora erythraea

<400> 9

Met Tyr Glu Gly Gly Phe Ala Glu Leu Tyr Asp Arg Phe Tyr Arg Gly
1 5 10 15

Arg Gly Lys Asp Tyr Ala Ala Glu Ala Ala Gln Val Ala Arg Leu Val
20 25 30

Arg Asp Arg Leu Pro Ser Ala Ser Ser Leu Leu Asp Val Ala Cys Gly
35 40 45

Thr Gly Thr His Leu Arg Arg Phe Ala Asp Leu Phe Asp Asp Val Thr
50 55 60

Gly Leu Glu Leu Ser Ala Ala Met Ile Glu Val Ala Arg Pro Gln Leu
65 70 75 80

Gly Gly Ile Pro Val Leu Gln Gly Asp Met Arg Asp Phe Ala Leu Asp
85 90 95

Arg Glu Phe Asp Ala Val Thr Cys Met Phe Ser Ser Ile Gly His Met
100 105 110

Arg Asp Gly Ala Glu Leu Asp Gln Ala Leu Ala Ser Phe Ala Arg His
115 120 125

Leu Ala Pro Gly Gly Val Val Val Val Glu Pro Trp Trp Phe Pro Glu
130 135 140

Asp Phe Leu Asp Gly Tyr Val Ala Gly Asp Val Val Arg Asp Gly Asp
145 150 155 160

Leu Thr Ile Ser Arg Val Ser His Ser Val Arg Ala Gly Gly Ala Thr
165 170 175

Arg Met Glu Ile His Trp Val Val Ala Asp Ala Val Asn Gly Pro Arg
180 185 190

His His Val Glu His Tyr Glu Ile Thr Leu Phe Glu Arg Gln Gln Tyr
195 200 205

Glu Lys Ala Phe Thr Ala Ala Gly Cys Ala Val Gln Tyr Leu Glu Gly
210 215 220

Gly Pro Ser Gly Arg Gly Leu Phe Val Gly Val Arg Gly
225 230 235

<210> 10

<211> 510

<212> PRT

<213> Saccharopolyspora erythraea

<400> 10

Met Arg Val Leu Ile Asp Asn Ala Arg Arg Gln Gln Ala Glu Pro Ser
1 5 10 15

Thr Thr Pro Gln Gly Glu Ser Met Gly Asp Arg Thr Gly Asp Arg Thr
20 25 30

Ile Pro Glu Ser Ser Gln Thr Ala Thr Arg Phe Leu Leu Gly Asp Gly
35 40 45

Gly Ile Pro Thr Ala Thr Ala Glu Thr His Asp Trp Leu Thr Arg Asn
50 55 60

Gly Ala Glu Gln Arg Leu Glu Val Ala Arg Val Pro Phe Ser Ala Met
65 70 75 80

Asp Arg Trp Ser Phe Gln Pro Glu Asp Gly Arg Leu Ala His Glu Ser
85 90 95

Gly Arg Phe Phe Ser Ile Glu Gly Leu His Val Arg Thr Asn Phe Gly
100 105 110

Trp Arg Arg Asp Trp Ile Gln Pro Ile Ile Val Gln Pro Glu Ile Gly
115 120 125

Phe Leu Gly Leu Ile Val Lys Glu Phe Asp Gly Val Leu His Val Leu
130 135 140

Ala Gln Ala Lys Ala Glu Pro Gly Asn Ile Asn Ala Val Gln Leu Ser
145 150 155 160

Pro Thr Leu Gln Ala Thr Arg Ser Asn Tyr Thr Gly Val His Arg Gly
165 170 175

Ser Lys Val Arg Phe Ile Glu Tyr Phe Asn Gly Thr Arg Pro Ser Arg
180 185 190

Ile Leu Val Asp Val Leu Gln Ser Glu Gln Gly Ala Trp Phe Leu Arg

195	200	205
Lys Arg Asn Arg Asn Met Val Val Glu Val Phe Asp Asp Leu Pro Glu 210 215 220		
His Pro Asn Phe Arg Trp Leu Thr Val Ala Gln Leu Arg Ala Met Leu 225 230 235 240		
His His Asp Asn Val Val Asn Met Asp Leu Arg Thr Val Leu Ala Cys 245 250 255		
Val Pro Thr Ala Val Glu Arg Asp Arg Ala Asp Asp Val Leu Ala Arg 260 265 270		
Leu Pro Glu Gly Ser Phe Gln Ala Arg Leu Leu His Ser Phe Ile Gly 275 280 285		
Ala Gly Thr Pro Ala Asn Asn Met Asn Ser Leu Leu Ser Trp Ile Ser 290 295 300		
Asp Val Arg Ala Arg Arg Glu Phe Val Gln Arg Gly Arg Pro Leu Pro 305 310 315 320		
Asp Ile Glu Arg Ser Gly Trp Ile Arg Arg Asp Asp Gly Ile Glu His 325 330 335		
Glu Glu Lys Lys Tyr Phe Asp Val Phe Gly Val Thr Val Ala Thr Ser 340 345 350		
Asp Arg Glu Val Asn Ser Trp Met Gln Pro Leu Leu Ser Pro Ala Asn 355 360 365		
Asn Gly Leu Leu Ala Leu Leu Val Lys Asp Ile Gly Gly Thr Leu His 370 375 380		
Ala Leu Val Gln Leu Arg Thr Glu Ala Gly Gly Met Asp Val Ala Glu 385 390 395 400		
Leu Ala Pro Thr Val His Cys Gln Pro Asp Asn Tyr Ala Asp Ala Pro 405 410 415		
Glu Glu Phe Arg Pro Ala Tyr Val Asp Tyr Val Leu Asn Val Pro Arg 420 425 430		
Ser Gln Val Arg Tyr Asp Ala Trp His Ser Glu Glu Gly Gly Arg Phe 435 440 445		
Tyr Arg Asn Glu Asn Arg Tyr Met Leu Ile Glu Val Pro Ala Asp Phe 450 455 460		
Asp Ala Ser Ala Ala Pro Asp His Arg Trp Met Thr Phe Asp Gln Ile 465 470 475 480		
Thr Tyr Leu Leu Gly His Ser His Tyr Val Asn Ile Gln Leu Arg Ser 485 490 495		
Ile Ile Ala Cys Ala Ser Ala Val Tyr Thr Arg Thr Ala Gly		

500

505

510

<210> 11

<211> 489

<212> PRT

<213> Saccharopolyspora erythraea

<400> 11

Met Asn Thr Thr Arg Thr Ala Thr Ala Gln Glu Ala Gly Val Ala Asp
 1 5 10 15

Ala Ala Arg Pro Asp Val Asp Arg Arg Ala Val Val Arg Ala Leu Ser
 20 25 30

Ser Glu Val Ser Arg Val Thr Gly Ala Gly Asp Gly Asp Ala Asp Val
 35 40 45

Gln Ala Ala Arg Leu Ala Asp Leu Ala Ala His Tyr Gly Ala His Pro
 50 55 60

Phe Thr Pro Leu Glu Gln Thr Arg Ala Arg Leu Gly Leu Asp Arg Ala
 65 70 75 80

Glu Phe Ala His Leu Leu Asp Leu Phe Gly Arg Ile Pro Asp Leu Gly
 85 90 95

Thr Ala Val Glu His Gly Pro Ala Gly Lys Tyr Trp Ser Asn Thr Ile
 100 105 110

Lys Pro Leu Asp Ala Ala Gly Ala Leu Asp Ala Ala Val Tyr Arg Lys
 115 120 125

Pro Ala Phe Pro Tyr Ser Val Gly Leu Tyr Pro Gly Pro Thr Cys Met
 130 135 140

Phe Arg Cys His Phe Cys Val Arg Val Thr Gly Ala Arg Tyr Glu Ala
 145 150 155 160

Ala Ser Val Pro Ala Gly Asn Glu Thr Leu Ala Ala Ile Ile Asp Glu
 165 170 175

Val Pro Thr Asp Asn Pro Lys Ala Met Tyr Met Ser Gly Gly Leu Glu
 180 185 190

Pro Leu Thr Asn Pro Gly Leu Gly Glu Leu Val Ser His Ala Ala Gly
 195 200 205

Arg Gly Phe Asp Leu Thr Val Tyr Thr Asn Ala Phe Ala Leu Thr Glu
 210 215 220

Gln Thr Leu Asn Arg Gln Pro Gly Leu Trp Glu Leu Gly Ala Ile Arg
 225 230 235 240

Thr Ser Leu Tyr Gly Leu Asn Asn Asp Glu Tyr Glu Thr Thr Thr Gly
 245 250 255

Lys Arg Gly Ala Phe Glu Arg Val Lys Lys Asn Leu Gln Gly Phe Leu

260										265										270													
Arg	Met	Arg	Ala	Glu	Arg	Asp	Ala	Pro	Ile	Arg	Leu	Gly	Phe	Asn	His																		
		275					280					285																					
Ile	Ile	Leu	Pro	Gly	Arg	Ala	Asp	Arg	Leu	Thr	Asp	Leu	Val	Asp	Phe																		
	290					295					300																						
Ile	Ala	Glu	Leu	Asn	Glu	Ser	Ser	Pro	Gln	Arg	Pro	Leu	Asp	Phe	Val																		
305				310					315						320																		
Thr	Val	Arg	Glu	Asp	Tyr	Ser	Gly	Arg	Asp	Asp	Gly	Arg	Leu	Ser	Asp																		
				325					330					335																			
Ser	Glu	Arg	Asn	Glu	Leu	Arg	Glu	Gly	Leu	Val	Arg	Phe	Val	Asp	Tyr																		
			340					345					350																				
Ala	Ala	Glu	Arg	Thr	Pro	Gly	Met	His	Ile	Asp	Leu	Gly	Tyr	Ala	Leu																		
		355					360					365																					
Glu	Ser	Leu	Arg	Arg	Gly	Val	Asp	Ala	Glu	Leu	Leu	Arg	Ile	Arg	Pro																		
	370					375					380																						
Glu	Thr	Met	Arg	Pro	Thr	Ala	His	Pro	Gln	Val	Ala	Val	Gln	Ile	Asp																		
385					390					395				400																			
Leu	Leu	Gly	Asp	Val	Tyr	Leu	Tyr	Arg	Glu	Ala	Gly	Phe	Pro	Glu	Leu																		
				405					410					415																			
Glu	Gly	Ala	Thr	Arg	Tyr	Ile	Ala	Gly	Arg	Val	Thr	Pro	Ser	Thr	Ser																		
			420					425					430																				
Leu	Arg	Glu	Val	Val	Glu	Asn	Phe	Val	Leu	Glu	Asn	Glu	Gly	Val	Gln																		
		435					440					445																					
Pro	Arg	Pro	Gly	Asp	Glu	Tyr	Phe	Leu	Asp	Gly	Phe	Asp	Gln	Ser	Val																		
	450					455					460																						
Thr	Ala	Arg	Leu	Asn	Gln	Leu	Glu	Arg	Asp	Ile	Ala	Asp	Gly	Trp	Glu																		
465					470					475				480																			
Asp	His	Arg	Gly	Phe	Leu	Arg	Gly	Arg																									
				485																													

<210> 12

<211> 193

<212> PRT

<213> Saccharopolyspora erythraea

<400> 12

Met	Ala	Gly	Gly	Phe	Glu	Phe	Thr	Pro	Asp	Pro	Lys	Gln	Asp	Arg	Arg
1				5					10					15	

Gly	Leu	Phe	Val	Ser	Pro	Leu	Gln	Asp	Glu	Ala	Phe	Val	Gly	Ala	Val
			20					25					30		

Gly His Arg Phe Pro Val Ala Gln Met Asn His Ile Val Ser Ala Arg
 35 40 45
 Gly Val Leu Arg Gly Leu His Phe Thr Thr Thr Pro Pro Gly Gln Cys
 50 55 60
 Lys Tyr Val Tyr Cys Ala Arg Gly Arg Ala Leu Asp Val Ile Val Asp
 65 70 75 80
 Ile Arg Val Gly Ser Pro Thr Phe Gly Lys Trp Asp Ala Val Glu Met
 85 90 95
 Asp Thr Glu His Phe Arg Ala Val Tyr Phe Pro Arg Gly Thr Ala His
 100 105 110
 Ala Phe Leu Ala Leu Glu Asp Asp Thr Leu Met Ser Tyr Leu Val Ser
 115 120 125
 Thr Pro Tyr Val Ala Glu Tyr Glu Gln Ala Ile Asp Pro Phe Asp Pro
 130 135 140
 Ala Leu Gly Leu Pro Trp Pro Ala Asp Leu Glu Val Val Leu Ser Asp
 145 150 155 160
 Arg Asp Thr Val Ala Val Asp Leu Glu Thr Ala Arg Arg Arg Gly Met
 165 170 175
 Leu Pro Asp Tyr Ala Asp Cys Leu Gly Glu Glu Pro Ala Ser Thr Gly
 180 185 190

Arg

<210> 13
 <211> 1206
 <212> DNA
 <213> Saccharopolyspora erythraea

<220>
 <221> CDS
 <222> (1)..(1203)
 <223> /function= "involved in the biosynthesis of
 desosamine" /gene= "eryCIV" /note= "SEQ ID No 6
 from 4837 to 6039"

<220>
 <221> mat_peptide
 <222> (1)

<400> 131
 atg aaa cgc gcg ctg acc gac ctg gcg atc ttc ggc ggc ccc gag gca 48
 Met Lys Arg Ala Leu Thr Asp Leu Ala Ile Phe Gly Gly Pro Glu Ala
 1 5 10 15
 ttc ctg cac acc ctc tac gtg ggc agg ccg acc gtc ggg gac cgg gag 96
 Phe Leu His Thr Leu Tyr Val Gly Arg Pro Thr Val Gly Asp Arg Glu
 20 25 30

cgg ttc ttc gcc cgc ctg gag tgg gcg ctg aac aac aac tgg ctg acc Arg Phe Phe Ala Arg Leu Glu Trp Ala Leu Asn Asn Asn Trp Leu Thr 35 40 45	144
aac ggc gga cca ctg gtg cgc gag ttc gag ggc cgg gtc gcc gac ctg Asn Gly Gly Pro Leu Val Arg Glu Phe Glu Gly Arg Val Ala Asp Leu 50 55 60	192
gcg ggt gtc cgc cac tgc gtg gcc acc tgc aac gcg acg gtc gcg ctg Ala Gly Val Arg His Cys Val Ala Thr Cys Asn Ala Thr Val Ala Leu 65 70 75 80	240
caa ctg gtg ctg cgc gcg agc gac gtg tcc ggc gag gtc gtc atg cct Gln Leu Val Leu Arg Ala Ser Asp Val Ser Gly Glu Val Val Met Pro 85 90 95	288
tcg atg acg ttc gcg gcc acc gcg cac gcg gcg agc tgg ctg ggg ctg Ser Met Thr Phe Ala Ala Thr Ala His Ala Ala Ser Trp Leu Gly Leu 100 105 110	336
gaa ccg gtg ttc tgc gac gtg gac ccc gag acc ggc ctg ctc gac ccc Glu Pro Val Phe Cys Asp Val Asp Pro Glu Thr Gly Leu Leu Asp Pro 115 120 125	384
gag cac gtc gcg tcg ctg gtg aca ccg cgg acg ggc gcg atc atc ggc Glu His Val Ala Ser Leu Val Thr Pro Arg Thr Gly Ala Ile Ile Gly 130 135 140	432
gtg cac ctg tgg ggc agg ccc gct ccg gtc gag gcg ctg gag aag atc Val His Leu Trp Gly Arg Pro Ala Pro Val Glu Ala Leu Glu Lys Ile 145 150 155 160	480
gcc gcc gag cac cag gtc aaa ctc ttc ttc gac gcc gcg cac gcg ctg Ala Ala Glu His Gln Val Lys Leu Phe Phe Asp Ala Ala His Ala Leu 165 170 175	528
ggc tgc acc gcc ggc ggg cgg ccg gtc ggc gcc ttc ggc aac gcc gag Gly Cys Thr Ala Gly Gly Arg Pro Val Gly Ala Phe Gly Asn Ala Glu 180 185 190	576
gtg ttc agc ttc cac gcc acg aag gcg gtc acc tcg ttc gag ggc ggc Val Phe Ser Phe His Ala Thr Lys Ala Val Thr Ser Phe Glu Gly Gly 195 200 205	624
gcc atc gtc acc gac gac ggg ctg ctg gcc gac cgc atc cgc gcc atg Ala Ile Val Thr Asp Asp Gly Leu Leu Ala Asp Arg Ile Arg Ala Met 210 215 220	672
cac aac ttc ggg atc gca ccg gac aag ctg gtg acc gat gtc ggc acc His Asn Phe Gly Ile Ala Pro Asp Lys Leu Val Thr Asp Val Gly Thr 225 230 235 240	720
aac ggc aag atg agc gag tgc gcc gcg gcg atg ggc ctc acc tcg ctc Asn Gly Lys Met Ser Glu Cys Ala Ala Ala Met Gly Leu Thr Ser Leu 245 250 255	768

gac gcc ttc gcc gag acc agg gtg cac aac cgc ctc aac cac gcg ctc	816
Asp Ala Phe Ala Glu Thr Arg Val His Asn Arg Leu Asn His Ala Leu	
260 265 270	
tac tcc gac gag ctc cgc gac gtg cgc ggc ata tcc gtg cac gcg ttc	864
Tyr Ser Asp Glu Leu Arg Asp Val Arg Gly Ile Ser Val His Ala Phe	
275 280 285	
gat cct ggc gag cag aac aac tac cag tac gtg atc atc tcg gtg gac	912
Asp Pro Gly Glu Gln Asn Asn Tyr Gln Tyr Val Ile Ile Ser Val Asp	
290 295 300	
tcc gcg gcc acc ggc atc gac cgc gac cag ttg cag gcg atc ctg cga	960
Ser Ala Ala Thr Gly Ile Asp Arg Asp Gln Leu Gln Ala Ile Leu Arg	
305 310 315 320	
gcg gag aag gtt gtg gca caa ccc tac ttc tcc ccc ggg tgc cac cag	1008
Ala Glu Lys Val Val Ala Gln Pro Tyr Phe Ser Pro Gly Cys His Gln	
325 330 335	
atg cag ccg tac cgg acc gag ccg ccg ctg cgg ctg gag aac acc gaa	1056
Met Gln Pro Tyr Arg Thr Glu Pro Pro Leu Arg Leu Glu Asn Thr Glu	
340 345 350	
cag ctc tcc gac cgg gtg ctc gcg ctg ccc acc ggc ccc gcg gtg tcc	1104
Gln Leu Ser Asp Arg Val Leu Ala Leu Pro Thr Gly Pro Ala Val Ser	
355 360 365	
agc gag gac atc cgg cgg gtg tgc gac atc atc cgg ctc gcc gcc acc	1152
Ser Glu Asp Ile Arg Arg Val Cys Asp Ile Ile Arg Leu Ala Ala Thr	
370 375 380	
agc ggc gag ctg atc aac gcg caa tgg gac cag agg acg cgc aac ggt	1200
Ser Gly Glu Leu Ile Asn Ala Gln Trp Asp Gln Arg Thr Arg Asn Gly	
385 390 395 400	
tcg tga	1206
Ser	

<210> 14

<211> 401

<212> PRT

<213> Saccharopolyspora erythraea

<400> 14

Met Lys Arg Ala Leu Thr Asp Leu Ala Ile Phe Gly Gly Pro Glu Ala
1 5 10 15

Phe Leu His Thr Leu Tyr Val Gly Arg Pro Thr Val Gly Asp Arg Glu
20 25 30

Arg Phe Phe Ala Arg Leu Glu Trp Ala Leu Asn Asn Asn Trp Leu Thr
35 40 45

Asn Gly Gly Pro Leu Val Arg Glu Phe Glu Gly Arg Val Ala Asp Leu
50 55 60

Ala	Gly	Val	Arg	His	Cys	Val	Ala	Thr	Cys	Asn	Ala	Thr	Val	Ala	Leu	65	70	75	80
Gln	Leu	Val	Leu	Arg	Ala	Ser	Asp	Val	Ser	Gly	Glu	Val	Val	Met	Pro	85	90	95	
Ser	Met	Thr	Phe	Ala	Ala	Thr	Ala	His	Ala	Ala	Ser	Trp	Leu	Gly	Leu	100	105	110	
Glu	Pro	Val	Phe	Cys	Asp	Val	Asp	Pro	Glu	Thr	Gly	Leu	Leu	Asp	Pro	115	120	125	
Glu	His	Val	Ala	Ser	Leu	Val	Thr	Pro	Arg	Thr	Gly	Ala	Ile	Ile	Gly	130	135	140	
Val	His	Leu	Trp	Gly	Arg	Pro	Ala	Pro	Val	Glu	Ala	Leu	Glu	Lys	Ile	145	150	155	160
Ala	Ala	Glu	His	Gln	Val	Lys	Leu	Phe	Phe	Asp	Ala	Ala	His	Ala	Leu	165	170	175	
Gly	Cys	Thr	Ala	Gly	Gly	Arg	Pro	Val	Gly	Ala	Phe	Gly	Asn	Ala	Glu	180	185	190	
Val	Phe	Ser	Phe	His	Ala	Thr	Lys	Ala	Val	Thr	Ser	Phe	Glu	Gly	Gly	195	200	205	
Ala	Ile	Val	Thr	Asp	Asp	Gly	Leu	Leu	Ala	Asp	Arg	Ile	Arg	Ala	Met	210	215	220	
His	Asn	Phe	Gly	Ile	Ala	Pro	Asp	Lys	Leu	Val	Thr	Asp	Val	Gly	Thr	225	230	235	240
Asn	Gly	Lys	Met	Ser	Glu	Cys	Ala	Ala	Ala	Met	Gly	Leu	Thr	Ser	Leu	245	250	255	
Asp	Ala	Phe	Ala	Glu	Thr	Arg	Val	His	Asn	Arg	Leu	Asn	His	Ala	Leu	260	265	270	
Tyr	Ser	Asp	Glu	Leu	Arg	Asp	Val	Arg	Gly	Ile	Ser	Val	His	Ala	Phe	275	280	285	
Asp	Pro	Gly	Glu	Gln	Asn	Asn	Tyr	Gln	Tyr	Val	Ile	Ile	Ser	Val	Asp	290	295	300	
Ser	Ala	Ala	Thr	Gly	Ile	Asp	Arg	Asp	Gln	Leu	Gln	Ala	Ile	Leu	Arg	305	310	315	320
Ala	Glu	Lys	Val	Val	Ala	Gln	Pro	Tyr	Phe	Ser	Pro	Gly	Cys	His	Gln	325	330	335	
Met	Gln	Pro	Tyr	Arg	Thr	Glu	Pro	Pro	Leu	Arg	Leu	Glu	Asn	Thr	Glu	340	345	350	
Gln	Leu	Ser	Asp	Arg	Val	Leu	Ala	Leu	Pro	Thr	Gly	Pro	Ala	Val	Ser	355	360	365	

Ser Glu Asp Ile Arg Arg Val Cys Asp Ile Ile Arg Leu Ala Ala Thr
 370 375 380

Ser Gly Glu Leu Ile Asn Ala Gln Trp Asp Gln Arg Thr Arg Asn Gly
 385 390 395 400

Ser

<210> 15
 <211> 6093
 <212> DNA
 <213> Streptomyces antibioticus

<220>
 <221> CDS
 <222> (184)..(1386)
 <223> /gene= "oleP1"

<220>
 <221> CDS
 <222> (1437)..(2714)
 <223> /function= "glycosylation of 8,
 8a-desoxyoleandolide" /gene= "oleG1"
 /transl_except= (pos: 1437...1439, aa: Met)

<220>
 <221> CDS
 <222> (2722)..(3999)
 <223> /function= "glycosylation of 8,
 8a-desoxyoleandolide" /gene= "oleG2"

<220>
 <221> CDS
 <222> (4810)..(5967)
 <223> /gene= "oleY"

<220>
 <221> mat_peptide
 <222> (184)

<400> 15
 gcatgccccg ctttcctccc cctctccgaa cgcacgcgacg acccgatccc cctcagggac 60
 cggtgaagga gcgtgttgca ctcacgcagg acatgcaagg cgtacagccc gaaccagcca 120
 gtgtcgaaca cgcgggcggac gcagctcgaa cagagcgaac ggcgacacgga agccgcccag 180
 gag atg gag gac agc gaa ctg ggg cgc cgc ctg cag atg ctc cgc ggc 228
 Met Glu Asp Ser Glu Leu Gly Arg Arg Leu Gln Met Leu Arg Gly
 1 5 10 15
 atg cag tgg gtc ttc ggc gcc aac ggc gat ccg tac gcc cgg ctg ctg 276
 Met Gln Trp Val Phe Gly Ala Asn Gly Asp Pro Tyr Ala Arg Leu Leu
 20 25 30

tgt ggc atg gag gat gac ccg tca cct ttc tac gac gcg ata cgg acc	324
Cys Gly Met Glu Asp Asp Pro Ser Pro Phe Tyr Asp Ala Ile Arg Thr	
35 40 45	
ctg ggc gag ctg cac cgg agc agg acc gga gcc tgg gtc acc gcc gac	372
Leu Gly Glu Leu His Arg Ser Arg Thr Gly Ala Trp Val Thr Ala Asp	
50 55 60	
ccc ggg ctc ggg ggc cgc atc ctc gcc gac cgg aag gct cgg tgc ccg	420
Pro Gly Leu Gly Gly Arg Ile Leu Ala Asp Arg Lys Ala Arg Cys Pro	
65 70 75	
gaa ggc tcg tgg ccg gtg cgg gcg aag acc gac ggg ctg gag cag tac	468
Glu Gly Ser Trp Pro Val Arg Ala Lys Thr Asp Gly Leu Glu Gln Tyr	
80 85 90 95	
gtg ctg ccc ggg cac cag gcg ttc ctg cgg ctg gag cgc gag gag gcc	516
Val Leu Pro Gly His Gln Ala Phe Leu Arg Leu Glu Arg Glu Glu Ala	
100 105 110	
gag cga ctg cgg gag gtc gcg gcg ccg gtg ctg ggg gcc gcg gcg gtc	564
Glu Arg Leu Arg Glu Val Ala Ala Pro Val Leu Gly Ala Ala Ala Val	
115 120 125	
gac gcg tgg cgc ccg ctg atc gac gag gtc tgc gcg ggg ctc gcg aag	612
Asp Ala Trp Arg Pro Leu Ile Asp Glu Val Cys Ala Gly Leu Ala Lys	
130 135 140	
ggg ctg ccg gac acg ttc gac ctg gtc gag gag tac gcg ggg ctg gtg	660
Gly Leu Pro Asp Thr Phe Asp Leu Val Glu Glu Tyr Ala Gly Leu Val	
145 150 155	
ccg gtc gag gtg ctg gcg cgg atc tgg ggc gtc ccg gag gag gac cgc	708
Pro Val Glu Val Leu Ala Arg Ile Trp Gly Val Pro Glu Glu Asp Arg	
160 165 170 175	
gcc cgg ttc ggg cgt gac tgc cgg gcg ctc gct ccc gcg ctg gac agc	756
Ala Arg Phe Gly Arg Asp Cys Arg Ala Leu Ala Pro Ala Leu Asp Ser	
180 185 190	
ctc ctg tgt ccc cag cag ttg gcg ctg agc aag gac atg gcg tcc gcc	804
Leu Leu Cys Pro Gln Gln Leu Ala Leu Ser Lys Asp Met Ala Ser Ala	
195 200 205	
ctg gag gac ctg cgt ctc ctc ttc gac ggc ctc gac gcg acg ccg cgc	852
Leu Glu Asp Leu Arg Leu Leu Phe Asp Gly Leu Asp Ala Thr Pro Arg	
210 215 220	
ctc gcc ggc ccc gcc gac ggt gac gga acg gcc gtg gcc atg ctc acc	900
Leu Ala Gly Pro Ala Asp Gly Asp Gly Thr Ala Val Ala Met Leu Thr	
225 230 235	
gtt ctg ctc tgc acg gag ccg gtg acc acg gcg atc ggg aac acc gtg	948
Val Leu Leu Cys Thr Glu Pro Val Thr Thr Ala Ile Gly Asn Thr Val	
240 245 250 255	
ctc ggg ctc ctt ccc ggg cag tgg ccc gtg ccc tgc acc ggc cgg gtg	996

Leu Gly Leu Leu Pro Gly Gln Trp Pro Val Pro Cys Thr Gly Arg Val	
260 265 270	
gct gcc ggg cag gtt gcc ggg cag gcg ctg cac cgg gcg gtg tcg tac	1044
Ala Ala Gly Gln Val Ala Gly Gln Ala Leu His Arg Ala Val Ser Tyr	
275 280 285	
cgt atc gcg acg cgg ttc gcc cgg gag gac ctg gag ttg gcg ggc tgc	1092
Arg Ile Ala Thr Arg Phe Ala Arg Glu Asp Leu Glu Ala Gly Cys	
290 295 300	
gag gtc aag tcc ggt gac gag gtg gtg gtc ctg gcc gga gcg atc ggc	1140
Glu Val Lys Ser Gly Asp Glu Val Val Val Leu Ala Gly Ala Ile Gly	
305 310 315	
cgg aac gga ccg tcc gca gcc gcc ccg cct gcc cca ccg ggc cca gcg	1188
Arg Asn Gly Pro Ser Ala Ala Ala Pro Pro Ala Pro Pro Gly Pro Ala	
320 325 330 335	
gcc ccg ccc gcc ccg tcg gtc ttc ggt gcc gcc gcc ttc gag aac gcg	1236
Ala Pro Pro Ala Pro Ser Val Phe Gly Ala Ala Ala Phe Glu Asn Ala	
340 345 350	
ctg gcc gaa ccc ctc gtc cgg gct gtg acg gga gcg gcc ctc cag gcc	1284
Leu Ala Glu Pro Leu Val Arg Ala Val Thr Gly Ala Ala Leu Gln Ala	
355 360 365	
ctc gcg gag ggg ccc ccc cgg ctg acg gcg gcg gga ccc gtc gta cga	1332
Leu Ala Glu Gly Pro Pro Arg Leu Thr Ala Ala Gly Pro Val Val Arg	
370 375 380	
cgg cgg cgt tcc cct gtc gtc ggc ggg ctg cac cgg gct ccg gtg gcc	1380
Arg Arg Arg Ser Pro Val Val Gly Gly Leu His Arg Ala Pro Val Ala	
385 390 395	
gcc gca tgagcatcgc gtcgaacggc gcgcgctcgg ccccccgcgc gccctgcgc	1436
Ala Ala	
400	
gtg atg atg acc acc ttc gcg gcc aac acg cac ttc cag ccg ctg gtt	1484
Met Met Met Thr Thr Phe Ala Ala Asn Thr His Phe Gln Pro Leu Val	
405 410 415	
ccc ctg gcc tgg gca ctg cgg aca gcc ggg cac gag gtg cgc gtg gtg	1532
Pro Leu Ala Trp Ala Leu Arg Thr Ala Gly His Glu Val Arg Val Val	
420 425 430	
agc cag ccc tcg ctg agc gac gtg gtg acg cag gcg ggg ctc acc tcg	1580
Ser Gln Pro Ser Leu Ser Asp Val Val Thr Gln Ala Gly Leu Thr Ser	
435 440 445	
gtc ccg gtg ggc acc gag gct ccg gtc gag cag ttc gcg gcg acc tgg	1628
Val Pro Val Gly Thr Glu Ala Pro Val Glu Gln Phe Ala Ala Thr Trp	
450 455 460 465	
ggc gac gat gcc tac atc ggc gtc aac agc atc gac ttc acc ggc aac	1676
Gly Asp Asp Ala Tyr Ile Gly Val Asn Ser Ile Asp Phe Thr Gly Asn	

470										475					480					
gac	ccc	ggc	ctg	tgg	acg	tgg	ccg	tac	ctc	ctg	ggc	atg	gag	acc	atg	1724				
Asp	Pro	Gly	Leu	Trp	Thr	Trp	Pro	Tyr	Leu	Leu	Gly	Met	Glu	Thr	Met					
		485						490					495							
ctg	gtg	ccg	gcc	ttc	tac	gag	ttg	ctg	aac	aac	gag	tcc	ttc	gtg	gac	1772				
Leu	Val	Pro	Ala	Phe	Tyr	Glu	Leu	Leu	Asn	Asn	Glu	Ser	Phe	Val	Asp					
		500						505				510								
ggc	gta	gtc	gag	ttc	gcc	cgt	gac	tgg	cgg	ccc	gac	ctg	gtg	atc	tgg	1820				
Gly	Val	Val	Glu	Phe	Ala	Arg	Asp	Trp	Arg	Pro	Asp	Leu	Val	Ile	Trp					
	515					520					525									
gag	ccg	ctg	acg	ttc	gcc	ggc	gcg	gtg	gcg	gcg	cgc	gtc	acc	ggc	gcg	1868				
Glu	Pro	Leu	Thr	Phe	Ala	Gly	Ala	Val	Ala	Ala	Arg	Val	Thr	Gly	Ala					
530					535					540					545					
gcc	cac	gcc	cgg	ctg	ccg	tgg	ggg	cag	gag	atc	acc	ctg	cgc	ggg	cgg	1916				
Ala	His	Ala	Arg	Leu	Pro	Trp	Gly	Gln	Glu	Ile	Thr	Leu	Arg	Gly	Arg					
				550					555					560						
cag	gcg	ttc	ctc	gcc	gag	cgt	gcc	ctg	caa	ccg	ttc	gag	cac	cgg	gag	1964				
Gln	Ala	Phe	Leu	Ala	Glu	Arg	Ala	Leu	Gln	Pro	Phe	Glu	His	Arg	Glu					
		565						570					575							
gat	ccc	acg	gcc	gag	tgg	ctg	ggc	cgc	atg	ctc	gac	cgg	tac	ggc	tgc	2012				
Asp	Pro	Thr	Ala	Glu	Trp	Leu	Gly	Arg	Met	Leu	Asp	Arg	Tyr	Gly	Cys					
		580					585					590								
tcg	ttc	gac	gag	gag	atg	gtc	acc	ggg	cag	tgg	acc	atc	gac	acg	ctg	2060				
Ser	Phe	Asp	Glu	Glu	Met	Val	Thr	Gly	Gln	Trp	Thr	Ile	Asp	Thr	Leu					
	595					600					605									
ccg	cgc	agc	atg	cgg	ctg	gag	ctg	tcc	gag	gag	ctg	cgc	acc	ctg	gac	2108				
Pro	Arg	Ser	Met	Arg	Leu	Glu	Leu	Ser	Glu	Glu	Leu	Arg	Thr	Leu	Asp					
610					615						620				625					
atg	cgg	tac	gtg	ccg	tac	aac	gga	ccg	gcg	gtc	gta	ccc	ccc	tgg	gtg	2156				
Met	Arg	Tyr	Val	Pro	Tyr	Asn	Gly	Pro	Ala	Val	Val	Pro	Pro	Trp	Val					
				630					635					640						
tgg	gaa	ccg	tgc	gag	cgg	ccc	cgg	gtc	tgt	ctg	acg	atc	ggc	acc	tcc	2204				
Trp	Glu	Pro	Cys	Glu	Arg	Pro	Arg	Val	Cys	Leu	Thr	Ile	Gly	Thr	Ser					
			645					650					655							
cag	cgt	gac	tcc	ggc	cgg	gac	cat	gtc	ccc	ctc	gac	cac	ctg	ctc	gac	2252				
Gln	Arg	Asp	Ser	Gly	Arg	Asp	His	Val	Pro	Leu	Asp	His	Leu	Leu	Asp					
		660					665					670								
tcc	ctc	gcc	gac	gtg	gac	gcg	gag	atc	gtg	gcc	acg	ctc	gac	acc	acc	2300				
Ser	Leu	Ala	Asp	Val	Asp	Ala	Glu	Ile	Val	Ala	Thr	Leu	Asp	Thr	Thr					
	675					680					685									
cag	cag	gag	cgc	ctg	cgg	ggc	gcg	gcc	ccc	ggc	aac	gtc	cgg	ctg	gtg	2348				
Gln	Gln	Glu	Arg	Leu	Arg	Gly	Ala	Ala	Pro	Gly	Asn	Val	Arg	Leu	Val					
690					695					700					705					

gac ttc gtc ccg ctg cac gcg ctg atg ccg acc tgc tgc gcg atc gtg	2396
Asp Phe Val Pro Leu His Ala Leu Met Pro Thr Cys Ser Ala Ile Val	
710 715 720	
cac cac ggt ggt ccg ggc acg tgg tgc acg gcg gcg ctc cac ggc gtc	2444
His His Gly Gly Pro Gly Thr Trp Ser Thr Ala Ala Leu His Gly Val	
725 730 735	
ccg cag atc atc ctg gac acc tgc tgg gac aca ccg gtg cgg gcg cag	2492
Pro Gln Ile Ile Leu Asp Thr Ser Trp Asp Thr Pro Val Arg Ala Gln	
740 745 750	
cgc atg cag caa ctc ggg gcg ggc ctg tgc atg ccg gtg ggg gaa ctg	2540
Arg Met Gln Gln Leu Gly Ala Gly Leu Ser Met Pro Val Gly Glu Leu	
755 760 765	
ggc gtc gag gcg ctg cgg gac cgg gtc ctg cgg ctg ctg ggg gag ccg	2588
Gly Val Glu Ala Leu Arg Asp Arg Val Leu Arg Leu Leu Gly Glu Pro	
770 775 780 785	
gag ttc cgc gcg ggc gcc gag cgg atc cgg gcc gag atg ctc gcg atg	2636
Glu Phe Arg Ala Gly Ala Glu Arg Ile Arg Ala Glu Met Leu Ala Met	
790 795 800	
ccc gcc ccc ggt gac gtc gta ccg gac ctg gaa cga ctc acc gcg gag	2684
Pro Ala Pro Gly Asp Val Val Pro Asp Leu Glu Arg Leu Thr Ala Glu	
805 810 815	
cat gcc acc ggc gcg atg gcg gga agg cgg tgagacg atg cgc gta ctg	2733
His Ala Thr Gly Ala Met Ala Gly Arg Arg Met Arg Val Leu	
820 825 830	
ctg acc tgc ttc gcc aac gac acc cac ttc cac ggg ctg gtg ccg ctg	2781
Leu Thr Cys Phe Ala Asn Asp Thr His Phe His Gly Leu Val Pro Leu	
835 840 845	
gcg tgg gcg ctg cgg gcc gcc ggg cac gaa gtc cgc gtg gcc agt cag	2829
Ala Trp Ala Leu Arg Ala Ala Gly His Glu Val Arg Val Ala Ser Gln	
850 855 860	
ccc gcc ctg tcc gac acg atc acc caa gcg gga ctg acc gcg gtg ccc	2877
Pro Ala Leu Ser Asp Thr Ile Thr Gln Ala Gly Leu Thr Ala Val Pro	
865 870 875	
gtg ggc cgg gac acc gcc ttc ctg gag ctg atg ggg gag atc ggc gcg	2925
Val Gly Arg Asp Thr Ala Phe Leu Glu Leu Met Gly Glu Ile Gly Ala	
880 885 890 895	
gac gtc cag aag tac tcc acc ggc atc gac ctg ggc gtc cgc gcg gag	2973
Asp Val Gln Lys Tyr Ser Thr Gly Ile Asp Leu Gly Val Arg Ala Glu	
900 905 910	
ctg acg agc tgg gag tac ctg ctc ggc atg cac acg acc ctg gtg ccc	3021
Leu Thr Ser Trp Glu Tyr Leu Leu Gly Met His Thr Thr Leu Val Pro	
915 920 925	

acg ttc tac tcg ctg gtc aac gac gag ccg ttc gtc gac ggg ctc gtc	3069
Thr Phe Tyr Ser Leu Val Asn Asp Glu Pro Phe Val Asp Gly Leu Val	
930 935 940	
gcg ctg acc cgg gcc tgg cgg ccc gac ctc atc ctg tgg gag cac ttc	3117
Ala Leu Thr Arg Ala Trp Arg Pro Asp Leu Ile Leu Trp Glu His Phe	
945 950 955	
agc ttc gcc ggg gcg ttg gcg gcg cgg gcc acc ggc acg ccc cac gcc	3165
Ser Phe Ala Gly Ala Leu Ala Ala Arg Ala Thr Gly Thr Pro His Ala	
960 965 970 975	
cgc gtg ctg tgg ggg tcg gac ctc atc gtc cgg ttc cgc cgg gac ttc	3213
Arg Val Leu Trp Gly Ser Asp Leu Ile Val Arg Phe Arg Arg Asp Phe	
980 985 990	
ctc gcg gag cgg gcg aac cgg ccc gcc gag cac cgc gag gac ccc atg	3261
Leu Ala Glu Arg Ala Asn Arg Pro Ala Glu His Arg Glu Asp Pro Met	
995 1000 1005	
gcg gag tgg ctg ggc tgg gcg gcc gaa cgg ctg ggc tcc acc ttc gac	3309
Ala Glu Trp Leu Gly Trp Ala Ala Glu Arg Leu Gly Ser Thr Phe Asp	
1010 1015 1020	
gag gag ctg gtg acc ggg cag tgg acg atc gac ccg ctg ccg cgg agc	3357
Glu Glu Leu Val Thr Gly Gln Trp Thr Ile Asp Pro Leu Pro Arg Ser	
1025 1030 1035	
atg cgg ctg ccc acc ggg acg acg acg gtg ccg atg cgg tac gtg ccg	3405
Met Arg Leu Pro Thr Gly Thr Thr Thr Val Pro Met Arg Tyr Val Pro	
1040 1045 1050 1055	
tac aac ggg cgg gcc gtg gtc ccc gca tgg gtc cgg cag cgt gcg cgg	3453
Tyr Asn Gly Arg Ala Val Val Pro Ala Trp Val Arg Gln Arg Ala Arg	
1060 1065 1070	
cgg ccc cgg atc tgc ctg acg ctc ggt gtg tcg gcc cgg cag acc ctg	3501
Arg Pro Arg Ile Cys Leu Thr Leu Gly Val Ser Ala Arg Gln Thr Leu	
1075 1080 1085	
ggc gac ggc gtg tcg ctg gcg gag gtg ctg gcc gcg ctg ggc gac gtg	3549
Gly Asp Gly Val Ser Leu Ala Glu Val Leu Ala Ala Leu Gly Asp Val	
1090 1095 1100	
gac gcg gag atc gtg gcc acg ctg gac gcc tcc cag cgc aag ctc ctg	3597
Asp Ala Glu Ile Val Ala Thr Leu Asp Ala Ser Gln Arg Lys Leu Leu	
1105 1110 1115	
ggg ccg gtg ccg gac aac gtc cgg ctg gtg gac ttc gtg ccc ctg cac	3645
Gly Pro Val Pro Asp Asn Val Arg Leu Val Asp Phe Val Pro Leu His	
1120 1125 1130 1135	
gcc ctg atg ccg acc tgt tcg gcg atc gtg cac cac ggc ggc gcc ggt	3693
Ala Leu Met Pro Thr Cys Ser Ala Ile Val His His Gly Gly Ala Gly	
1140 1145 1150	
acc tgg ctg acg gcc gcc gtc cac ggc gtc ccg cag atc gtc ctc ggt	3741

Thr Trp Leu Thr Ala Ala Val His Gly Val Pro Gln Ile Val Leu Gly	
1155 1160 1165	
gac ctc tgg gac aac ctg ctg cgc gcc cgg cag aca cag gcc gcg ggc	3789
Asp Leu Trp Asp Asn Leu Leu Arg Ala Arg Gln Thr Gln Ala Ala Gly	
1170 1175 1180	
gcg ggc ctg ttc atc cat ccg tcc gag gtc acc gcg gcc ggg ctc ggt	3837
Ala Gly Leu Phe Ile His Pro Ser Glu Val Thr Ala Ala Gly Leu Gly	
1185 1190 1195	
gag ggc gtg cgc cgg gtg ctg acg gac cct tcc atc cgg gcc gcc gca	3885
Glu Gly Val Arg Arg Val Leu Thr Asp Pro Ser Ile Arg Ala Ala Ala	
1200 1205 1210 1215	
cag cgc gtc cgg gac gag atg aat gca gag ccg acg ccg ggc gag gtc	3933
Gln Arg Val Arg Asp Glu Met Asn Ala Glu Pro Thr Pro Gly Glu Val	
1220 1225 1230	
gtc acg gtg ctg gag cgg ctc gcc gcg agc ggc gga cgc gga cga gga	3981
Val Thr Val Leu Glu Arg Leu Ala Ala Ser Gly Gly Arg Gly Arg Gly	
1235 1240 1245	
ggc ggc aac cat gcg ggc tgacacggag ccgaccacg ggtacgagga	4029
Gly Gly Asn His Ala Gly	
1250	
cgagttcgcc gagatctacg acgccgtgta ccggggccgg ggcaaggact acgccggcga	4089
ggcgaaggac gtggcggacc tcgtgcgcga ccgggtgccc gacgcgtcct ccctcctgga	4149
cgtggcctgc ggcacgggcg cgcacctgcg gcacttcgcc acgctcttcg acgacgcccg	4209
cggtctcgaa ctgtccgcga gcatgctgga catcgcccgc tcccgcatgc cgggcgtgcc	4269
gctgcaccaa ggggacatgc gatccttcga cctggggcca cgcgtctccg cggtcacctg	4329
catgttcagc tccgtcggcc acctggccac caccgccgaa ctcgacgcga cgctgcggtg	4389
cttcgcccgg cacaccggc ccggcgccgt ggccgtcatc gaaccgtggt ggttcccga	4449
gaccttcacc gacggctacg tggcgggtga catcgtacgc gtcgacggcc ggaccatctc	4509
ccgggtgtcc cactcggtag gggacggcgg cgccaccgc atggagatcc actacgtgat	4569
cgccgacgcc gagcacggtc cccggcacct ggtcgagcac caccgcatca cgctgttccc	4629
gcggcatgcg tacacggccg cgtacgagaa ggccgggctac accgtcgagt acctcgacgg	4689
cgggccctcg ggccgggggc tgttcgtcgg caccggacg tgaaccgcgc cgcgacccgc	4749
ccgatcacc tgctcaacgc cgttcacacg gatcaccgga ccacgcgaag gacctttcac	4809
atg tcg tac gac gac cac gcg gtg ctg gaa gcg ata ctg cgg tgc gcc	4857
Met Ser Tyr Asp Asp His Ala Val Leu Glu Ala Ile Leu Arg Cys Ala	
1255 1260 1265	

gga ggt gac gag cgc ttc ctg ctg aac acc gtc gag gaa tgg gga gcc	4905
Gly Gly Asp Glu Arg Phe Leu Leu Asn Thr Val Glu Glu Trp Gly Ala	
1270 1275 1280 1285	
gcc gag atc acc gcg gcg ctc gtg gac gag ttg ctg ttc cgc tgc gag	4953
Ala Glu Ile Thr Ala Ala Leu Val Asp Glu Leu Leu Phe Arg Cys Glu	
1290 1295 1300	
atc ccg cag gtg ggc ggt gag gcg ttc atc ggc ctg gac gtc ctg cac	5001
Ile Pro Gln Val Gly Gly Glu Ala Phe Ile Gly Leu Asp Val Leu His	
1305 1310 1315	
ggc gcc gac cgg atc agc cat gtg ctg cag gtg acg gac ggc aag ccg	5049
Gly Ala Asp Arg Ile Ser His Val Leu Gln Val Thr Asp Gly Lys Pro	
1320 1325 1330	
gtc acg tcg gcg gaa ccg gcc ggc cag gaa ctg ggc ggc cgt acc tgg	5097
Val Thr Ser Ala Glu Pro Ala Gly Gln Glu Leu Gly Gly Arg Thr Trp	
1335 1340 1345	
agt tca cgc tca gcg acc ctc ctg cgg gag ctg ttc ggc ccg ccg tcc	5145
Ser Ser Arg Ser Ala Thr Leu Leu Arg Glu Leu Phe Gly Pro Pro Ser	
1350 1355 1360 1365	
ggc cgc acc gcg ggg ggc ttc ggc gtc tcc ttc ctg ccc gac ctg cgc	5193
Gly Arg Thr Ala Gly Gly Phe Gly Val Ser Phe Leu Pro Asp Leu Arg	
1370 1375 1380	
ggc ccg cgg acc atg gag ggc gcg gcc ctg gcc gcc cgc gcc acc aac	5241
Gly Pro Arg Thr Met Glu Gly Ala Ala Leu Ala Ala Arg Ala Thr Asn	
1385 1390 1395	
gtg gtg ctg cac gcg acg acc aac gag acg ccc cca ctg gac cgg ctg	5289
Val Val Leu His Ala Thr Thr Asn Glu Thr Pro Pro Leu Asp Arg Leu	
1400 1405 1410	
gcc ctg cgc tac gag tcc gac aag tgg ggc ggc gtc cac tgg ttc acc	5337
Ala Leu Arg Tyr Glu Ser Asp Lys Trp Gly Gly Val His Trp Phe Thr	
1415 1420 1425	
ggc cac tac gac cgg cac ctg cgg gcc gtg cgc gac cag gcg gtg cgg	5385
Gly His Tyr Asp Arg His Leu Arg Ala Val Arg Asp Gln Ala Val Arg	
1430 1435 1440 1445	
atc ctg gag atc ggc atc ggc ggc tac gac gac ctg ctg ccg agc ggc	5433
Ile Leu Glu Ile Gly Ile Gly Gly Tyr Asp Asp Leu Leu Pro Ser Gly	
1450 1455 1460	
gcc tca ctg aag atg tgg aag cgc tac ttc ccg cgc ggc ctg gtc ttc	5481
Ala Ser Leu Lys Met Trp Lys Arg Tyr Phe Pro Arg Gly Leu Val Phe	
1465 1470 1475	
ggc gtg gac atc ttc gac agt cgg cgt gcg acc agc cgc gtg tca aga	5529
Gly Val Asp Ile Phe Asp Ser Arg Arg Ala Thr Ser Arg Val Ser Arg	
1480 1485 1490	
cgc tcc gcg gcc cgg cag gac gac ccg gag ttc atg cgc cgc gtc gcc	5577

Arg Ser Ala Ala Arg Gln Asp Asp Pro Glu Phe Met Arg Arg Val Ala
 1495 1500 1505
 gag gag cac ggg ccg ttc gac gtc atc atc gac gac ggc agc cac atc 5625
 Glu Glu His Gly Pro Phe Asp Val Ile Ile Asp Asp Gly Ser His Ile
 1510 1515 1520 1525
 aac gca cac atg cgg acg tcg ttc tcg gtg atg ttc ccc cac ctg cgc 5673
 Asn Ala His Met Arg Thr Ser Phe Ser Val Met Phe Pro His Leu Arg
 1530 1535 1540
 aac ggc ggc ttc tac gtc atc gag gac acc ttc acc tcc tac tgg ccc 5721
 Asn Gly Gly Phe Tyr Val Ile Glu Asp Thr Phe Thr Ser Tyr Trp Pro
 1545 1550 1555
 ggg tac gga ggg cca tcc gga gcc cgg tgc ccg tcc gga aca acc gcg 5769
 Gly Tyr Gly Gly Pro Ser Gly Ala Arg Cys Pro Ser Gly Thr Thr Ala
 1560 1565 1570
 ctg gag atg gtc aag gga ctg atc gac tcg gtg cac tac gag gag cgg 5817
 Leu Glu Met Val Lys Gly Leu Ile Asp Ser Val His Tyr Glu Glu Arg
 1575 1580 1585
 ccg gac ggc gcg gcc acg gcc gac tac atc gcc agg aac ctc gtc ggg 5865
 Pro Asp Gly Ala Ala Thr Ala Asp Tyr Ile Ala Arg Asn Leu Val Gly
 1590 1595 1600 1605
 ctg cac gcc tac caa acg acc tcg tct tcc tcg aga agg gcg atc aac 5913
 Leu His Ala Tyr Gln Thr Thr Ser Ser Ser Ser Arg Arg Ala Ile Asn
 1610 1615 1620
 aag gag ggc ggc atc ccc cac acc gtg ccc cgg gag ccg ttc tgg aac 5961
 Lys Glu Gly Gly Ile Pro His Thr Val Pro Arg Glu Pro Phe Trp Asn
 1625 1630 1635
 gac aac tagccacggc cgcaaccaga gccggaaacc gcaccactgt ccgcgccacc 6017
 Asp Asn
 tcggaaccac ctccagcaaa ggacacaccg ctgtgaccga tacgcacacc ggaccgacac 6077
 cggccgacgc ggtacc 6093

<210> 16
 <211> 401
 <212> PRT
 <213> Streptomyces antibioticus

<400> 16
 Met Glu Asp Ser Glu Leu Gly Arg Arg Leu Gln Met Leu Arg Gly Met
 1 5 10 15
 Gln Trp Val Phe Gly Ala Asn Gly Asp Pro Tyr Ala Arg Leu Leu Cys
 20 25 30
 Gly Met Glu Asp Asp Pro Ser Pro Phe Tyr Asp Ala Ile Arg Thr Leu
 35 40 45

Gly Glu Leu His Arg Ser Arg Thr Gly Ala Trp Val Thr Ala Asp Pro
 50 55 60
 Gly Leu Gly Gly Arg Ile Leu Ala Asp Arg Lys Ala Arg Cys Pro Glu
 65 70 75 80
 Gly Ser Trp Pro Val Arg Ala Lys Thr Asp Gly Leu Glu Gln Tyr Val
 85 90 95
 Leu Pro Gly His Gln Ala Phe Leu Arg Leu Glu Arg Glu Glu Ala Glu
 100 105 110
 Arg Leu Arg Glu Val Ala Ala Pro Val Leu Gly Ala Ala Ala Val Asp
 115 120 125
 Ala Trp Arg Pro Leu Ile Asp Glu Val Cys Ala Gly Leu Ala Lys Gly
 130 135 140
 Leu Pro Asp Thr Phe Asp Leu Val Glu Glu Tyr Ala Gly Leu Val Pro
 145 150 155 160
 Val Glu Val Leu Ala Arg Ile Trp Gly Val Pro Glu Glu Asp Arg Ala
 165 170 175
 Arg Phe Gly Arg Asp Cys Arg Ala Leu Ala Pro Ala Leu Asp Ser Leu
 180 185 190
 Leu Cys Pro Gln Gln Leu Ala Leu Ser Lys Asp Met Ala Ser Ala Leu
 195 200 205
 Glu Asp Leu Arg Leu Leu Phe Asp Gly Leu Asp Ala Thr Pro Arg Leu
 210 215 220
 Ala Gly Pro Ala Asp Gly Asp Gly Thr Ala Val Ala Met Leu Thr Val
 225 230 235 240
 Leu Leu Cys Thr Glu Pro Val Thr Thr Ala Ile Gly Asn Thr Val Leu
 245 250 255
 Gly Leu Leu Pro Gly Gln Trp Pro Val Pro Cys Thr Gly Arg Val Ala
 260 265 270
 Ala Gly Gln Val Ala Gly Gln Ala Leu His Arg Ala Val Ser Tyr Arg
 275 280 285
 Ile Ala Thr Arg Phe Ala Arg Glu Asp Leu Glu Leu Ala Gly Cys Glu
 290 295 300
 Val Lys Ser Gly Asp Glu Val Val Val Leu Ala Gly Ala Ile Gly Arg
 305 310 315 320
 Asn Gly Pro Ser Ala Ala Ala Pro Pro Ala Pro Pro Gly Pro Ala Ala
 325 330 335
 Pro Pro Ala Pro Ser Val Phe Gly Ala Ala Ala Phe Glu Asn Ala Leu
 340 345 350

Ala Glu Pro Leu Val Arg Ala Val Thr Gly Ala Ala Leu Gln Ala Leu
355 360 365

Ala Glu Gly Pro Pro Arg Leu Thr Ala Ala Gly Pro Val Val Arg Arg
370 375 380

Arg Arg Ser Pro Val Val Gly Gly Leu His Arg Ala Pro Val Ala Ala
385 390 395 400

Ala

<210> 17

<211> 426

<212> PRT

<213> Streptomyces antibioticus

<400> 17

Met Met Met Thr Thr Phe Ala Ala Asn Thr His Phe Gln Pro Leu Val
1 5 10 15

Pro Leu Ala Trp Ala Leu Arg Thr Ala Gly His Glu Val Arg Val Val
20 25 30

Ser Gln Pro Ser Leu Ser Asp Val Val Thr Gln Ala Gly Leu Thr Ser
35 40 45

Val Pro Val Gly Thr Glu Ala Pro Val Glu Gln Phe Ala Ala Thr Trp
50 55 60

Gly Asp Asp Ala Tyr Ile Gly Val Asn Ser Ile Asp Phe Thr Gly Asn
65 70 75 80

Asp Pro Gly Leu Trp Thr Trp Pro Tyr Leu Leu Gly Met Glu Thr Met
85 90 95

Leu Val Pro Ala Phe Tyr Glu Leu Leu Asn Asn Glu Ser Phe Val Asp
100 105 110

Gly Val Val Glu Phe Ala Arg Asp Trp Arg Pro Asp Leu Val Ile Trp
115 120 125

Glu Pro Leu Thr Phe Ala Gly Ala Val Ala Ala Arg Val Thr Gly Ala
130 135 140

Ala His Ala Arg Leu Pro Trp Gly Gln Glu Ile Thr Leu Arg Gly Arg
145 150 155 160

Gln Ala Phe Leu Ala Glu Arg Ala Leu Gln Pro Phe Glu His Arg Glu
165 170 175

Asp Pro Thr Ala Glu Trp Leu Gly Arg Met Leu Asp Arg Tyr Gly Cys
180 185 190

Ser Phe Asp Glu Glu Met Val Thr Gly Gln Trp Thr Ile Asp Thr Leu
195 200 205

Pro Arg Ser Met Arg Leu Glu Leu Ser Glu Glu Leu Arg Thr Leu Asp
 210 215 220
 Met Arg Tyr Val Pro Tyr Asn Gly Pro Ala Val Val Pro Pro Trp Val
 225 230 235 240
 Trp Glu Pro Cys Glu Arg Pro Arg Val Cys Leu Thr Ile Gly Thr Ser
 245 250 255
 Gln Arg Asp Ser Gly Arg Asp His Val Pro Leu Asp His Leu Leu Asp
 260 265 270
 Ser Leu Ala Asp Val Asp Ala Glu Ile Val Ala Thr Leu Asp Thr Thr
 275 280 285
 Gln Gln Glu Arg Leu Arg Gly Ala Ala Pro Gly Asn Val Arg Leu Val
 290 295 300
 Asp Phe Val Pro Leu His Ala Leu Met Pro Thr Cys Ser Ala Ile Val
 305 310 315 320
 His His Gly Gly Pro Gly Thr Trp Ser Thr Ala Ala Leu His Gly Val
 325 330 335
 Pro Gln Ile Ile Leu Asp Thr Ser Trp Asp Thr Pro Val Arg Ala Gln
 340 345 350
 Arg Met Gln Gln Leu Gly Ala Gly Leu Ser Met Pro Val Gly Glu Leu
 355 360 365
 Gly Val Glu Ala Leu Arg Asp Arg Val Leu Arg Leu Leu Gly Glu Pro
 370 375 380
 Glu Phe Arg Ala Gly Ala Glu Arg Ile Arg Ala Glu Met Leu Ala Met
 385 390 395 400
 Pro Ala Pro Gly Asp Val Val Pro Asp Leu Glu Arg Leu Thr Ala Glu
 405 410 415
 His Ala Thr Gly Ala Met Ala Gly Arg Arg
 420 425

<210> 18

<211> 426

<212> PRT

<213> Streptomyces antibioticus

<400> 18

Met Arg Val Leu Leu Thr Cys Phe Ala Asn Asp Thr His Phe His Gly
 1 5 10 15

Leu Val Pro Leu Ala Trp Ala Leu Arg Ala Ala Gly His Glu Val Arg
 20 25 30

Val Ala Ser Gln Pro Ala Leu Ser Asp Thr Ile Thr Gln Ala Gly Leu

35					40					45					
Thr	Ala	Val	Pro	Val	Gly	Arg	Asp	Thr	Ala	Phe	Leu	Glu	Leu	Met	Gly
50						55					60				
Glu	Ile	Gly	Ala	Asp	Val	Gln	Lys	Tyr	Ser	Thr	Gly	Ile	Asp	Leu	Gly
65					70					75					80
Val	Arg	Ala	Glu	Leu	Thr	Ser	Trp	Glu	Tyr	Leu	Leu	Gly	Met	His	Thr
				85					90					95	
Thr	Leu	Val	Pro	Thr	Phe	Tyr	Ser	Leu	Val	Asn	Asp	Glu	Pro	Phe	Val
			100					105					110		
Asp	Gly	Leu	Val	Ala	Leu	Thr	Arg	Ala	Trp	Arg	Pro	Asp	Leu	Ile	Leu
		115					120					125			
Trp	Glu	His	Phe	Ser	Phe	Ala	Gly	Ala	Leu	Ala	Ala	Arg	Ala	Thr	Gly
	130					135						140			
Thr	Pro	His	Ala	Arg	Val	Leu	Trp	Gly	Ser	Asp	Leu	Ile	Val	Arg	Phe
145					150					155					160
Arg	Arg	Asp	Phe	Leu	Ala	Glu	Arg	Ala	Asn	Arg	Pro	Ala	Glu	His	Arg
				165					170					175	
Glu	Asp	Pro	Met	Ala	Glu	Trp	Leu	Gly	Trp	Ala	Ala	Glu	Arg	Leu	Gly
			180					185					190		
Ser	Thr	Phe	Asp	Glu	Glu	Leu	Val	Thr	Gly	Gln	Trp	Thr	Ile	Asp	Pro
		195					200						205		
Leu	Pro	Arg	Ser	Met	Arg	Leu	Pro	Thr	Gly	Thr	Thr	Thr	Val	Pro	Met
	210					215					220				
Arg	Tyr	Val	Pro	Tyr	Asn	Gly	Arg	Ala	Val	Val	Pro	Ala	Trp	Val	Arg
225					230					235					240
Gln	Arg	Ala	Arg	Arg	Pro	Arg	Ile	Cys	Leu	Thr	Leu	Gly	Val	Ser	Ala
				245					250					255	
Arg	Gln	Thr	Leu	Gly	Asp	Gly	Val	Ser	Leu	Ala	Glu	Val	Leu	Ala	Ala
			260					265					270		
Leu	Gly	Asp	Val	Asp	Ala	Glu	Ile	Val	Ala	Thr	Leu	Asp	Ala	Ser	Gln
		275					280					285			
Arg	Lys	Leu	Leu	Gly	Pro	Val	Pro	Asp	Asn	Val	Arg	Leu	Val	Asp	Phe
	290					295					300				
Val	Pro	Leu	His	Ala	Leu	Met	Pro	Thr	Cys	Ser	Ala	Ile	Val	His	His
305					310					315					320
Gly	Gly	Ala	Gly	Thr	Trp	Leu	Thr	Ala	Ala	Val	His	Gly	Val	Pro	Gln
				325					330					335	
Ile	Val	Leu	Gly	Asp	Leu	Trp	Asp	Asn	Leu	Leu	Arg	Ala	Arg	Gln	Thr

340 345 350
 Gln Ala Ala Gly Ala Gly Leu Phe Ile His Pro Ser Glu Val Thr Ala
 355 360 365
 Ala Gly Leu Gly Glu Gly Val Arg Arg Val Leu Thr Asp Pro Ser Ile
 370 375 380
 Arg Ala Ala Ala Gln Arg Val Arg Asp Glu Met Asn Ala Glu Pro Thr
 385 390 395 400
 Pro Gly Glu Val Val Thr Val Leu Glu Arg Leu Ala Ala Ser Gly Gly
 405 410 415
 Arg Gly Arg Gly Gly Gly Asn His Ala Gly
 420 425

<210> 19

<211> 386

<212> PRT

<213> Streptomyces antibioticus

<400> 19

Met Ser Tyr Asp Asp His Ala Val Leu Glu Ala Ile Leu Arg Cys Ala
 1 5 10 15
 Gly Gly Asp Glu Arg Phe Leu Leu Asn Thr Val Glu Glu Trp Gly Ala
 20 25 30
 Ala Glu Ile Thr Ala Ala Leu Val Asp Glu Leu Leu Phe Arg Cys Glu
 35 40 45
 Ile Pro Gln Val Gly Gly Glu Ala Phe Ile Gly Leu Asp Val Leu His
 50 55 60
 Gly Ala Asp Arg Ile Ser His Val Leu Gln Val Thr Asp Gly Lys Pro
 65 70 75 80
 Val Thr Ser Ala Glu Pro Ala Gly Gln Glu Leu Gly Gly Arg Thr Trp
 85 90 95
 Ser Ser Arg Ser Ala Thr Leu Leu Arg Glu Leu Phe Gly Pro Pro Ser
 100 105 110
 Gly Arg Thr Ala Gly Gly Phe Gly Val Ser Phe Leu Pro Asp Leu Arg
 115 120 125
 Gly Pro Arg Thr Met Glu Gly Ala Ala Leu Ala Ala Arg Ala Thr Asn
 130 135 140
 Val Val Leu His Ala Thr Thr Asn Glu Thr Pro Pro Leu Asp Arg Leu
 145 150 155 160
 Ala Leu Arg Tyr Glu Ser Asp Lys Trp Gly Gly Val His Trp Phe Thr
 165 170 175

Gly His Tyr Asp Arg His Leu Arg Ala Val Arg Asp Gln Ala Val Arg
 180 185 190
 Ile Leu Glu Ile Gly Ile Gly Gly Tyr Asp Asp Leu Leu Pro Ser Gly
 195 200 205
 Ala Ser Leu Lys Met Trp Lys Arg Tyr Phe Pro Arg Gly Leu Val Phe
 210 215 220
 Gly Val Asp Ile Phe Asp Ser Arg Arg Ala Thr Ser Arg Val Ser Arg
 225 230 235 240
 Arg Ser Ala Ala Arg Gln Asp Asp Pro Glu Phe Met Arg Arg Val Ala
 245 250 255
 Glu Glu His Gly Pro Phe Asp Val Ile Ile Asp Asp Gly Ser His Ile
 260 265 270
 Asn Ala His Met Arg Thr Ser Phe Ser Val Met Phe Pro His Leu Arg
 275 280 285
 Asn Gly Gly Phe Tyr Val Ile Glu Asp Thr Phe Thr Ser Tyr Trp Pro
 290 295 300
 Gly Tyr Gly Gly Pro Ser Gly Ala Arg Cys Pro Ser Gly Thr Thr Ala
 305 310 315 320
 Leu Glu Met Val Lys Gly Leu Ile Asp Ser Val His Tyr Glu Glu Arg
 325 330 335
 Pro Asp Gly Ala Ala Thr Ala Asp Tyr Ile Ala Arg Asn Leu Val Gly
 340 345 350
 Leu His Ala Tyr Gln Thr Thr Ser Ser Ser Arg Arg Ala Ile Asn
 355 360 365
 Lys Glu Gly Gly Ile Pro His Thr Val Pro Arg Glu Pro Phe Trp Asn
 370 375 380
 Asp Asn
 385

<210> 20
 <211> 738
 <212> DNA
 <213> Streptomyces antibioticus

<220>
 <221> CDS
 <222> (1)..(738)
 <223> /gene= "oleM" /note= "SEQ ID No. 15 from 3992 to 4729"

<220>
 <221> mat_peptide
 <222> (1)

<400> 20
atg cgg gct gac acg gag ccg acc acc ggg tac gag gac gag ttc gcc 48
Met Arg Ala Asp Thr Glu Pro Thr Thr Gly Tyr Glu Asp Glu Phe Ala
1 5 10 15

gag atc tac gac gcc gtg tac ccg ggc ccg ggc aag gac tac gcc ggc 96
Glu Ile Tyr Asp Ala Val Tyr Arg Gly Arg Gly Lys Asp Tyr Ala Gly
20 25 30

gag gcg aag gac gtg gcg gac ctc gtg cgc gac ccg gtg ccg gac gcg 144
Glu Ala Lys Asp Val Ala Asp Leu Val Arg Asp Arg Val Pro Asp Ala
35 40 45

tcc tcc ctc ctg gac gtg gcc tgc ggc acc ggc gcg cac ctg ccg cac 192
Ser Ser Leu Leu Asp Val Ala Cys Gly Thr Gly Ala His Leu Arg His
50 55 60

ttc gcc acc ctc ttc gac gac gcc cgc ggt ctc gaa ctg tcc gcg agc 240
Phe Ala Thr Leu Phe Asp Asp Ala Arg Gly Leu Glu Leu Ser Ala Ser
65 70 75 80

atg ctg gac atc gcc cgc tcc cgc atg ccg ggc gtg ccg ctg cac caa 288
Met Leu Asp Ile Ala Arg Ser Arg Met Pro Gly Val Pro Leu His Gln
85 90 95

ggg gac atg cga tcc ttc gac ctg ggg cca cgc gtc tcc gcg gtc acc 336
Gly Asp Met Arg Ser Phe Asp Leu Gly Pro Arg Val Ser Ala Val Thr
100 105 110

tgc atg ttc agc tcc gtc ggc cac ctg gcc acc acc gcc gaa ctc gac 384
Cys Met Phe Ser Ser Val Gly His Leu Ala Thr Thr Ala Glu Leu Asp
115 120 125

gcg acc ctg ccg tgc ttc gcc ccg cac acc ccg ccc ggc ggc gtg gcc 432
Ala Thr Leu Arg Cys Phe Ala Arg His Thr Arg Pro Gly Gly Val Ala
130 135 140

gtc atc gaa ccg tgg tgg ttc ccg gag acc ttc acc gac ggc tac gtg 480
Val Ile Glu Pro Trp Trp Phe Pro Glu Thr Phe Thr Asp Gly Tyr Val
145 150 155 160

gcg ggt gac atc gta cgc gtc gac ggc ccg acc atc tcc ccg gtg tcc 528
Ala Gly Asp Ile Val Arg Val Asp Gly Arg Thr Ile Ser Arg Val Ser
165 170 175

cac tcg gta ccg gac ggc ggc gcc acc cgc atg gag atc cac tac gtg 576
His Ser Val Arg Asp Gly Gly Ala Thr Arg Met Glu Ile His Tyr Val
180 185 190

atc gcc gac gcc gag cac ggt ccc ccg cac ctg gtc gag cac cac cgc 624
Ile Ala Asp Ala Glu His Gly Pro Arg His Leu Val Glu His His Arg
195 200 205

atc acc ctg ttc ccg ccg cat gcg tac acc gcc gcg tac gag aag gcg 672
Ile Thr Leu Phe Pro Arg His Ala Tyr Thr Ala Ala Tyr Glu Lys Ala
210 215 220

ggc tac acc gtc gag tac ctc gac ggc ggg ccc tcg ggc cgg ggg ctg 720
 Gly Tyr Thr Val Glu Tyr Leu Asp Gly Gly Pro Ser Gly Arg Gly Leu
 225 230 235 240

ttc gtc ggc acc cgg acg 738
 Phe Val Gly Thr Arg Thr
 245

<210> 21
 <211> 246
 <212> PRT
 <213> Streptomyces antibioticus

<400> 21
 Met Arg Ala Asp Thr Glu Pro Thr Thr Gly Tyr Glu Asp Glu Phe Ala
 1 5 10 15

Glu Ile Tyr Asp Ala Val Tyr Arg Gly Arg Gly Lys Asp Tyr Ala Gly
 20 25 30

Glu Ala Lys Asp Val Ala Asp Leu Val Arg Asp Arg Val Pro Asp Ala
 35 40 45

Ser Ser Leu Leu Asp Val Ala Cys Gly Thr Gly Ala His Leu Arg His
 50 55 60

Phe Ala Thr Leu Phe Asp Asp Ala Arg Gly Leu Glu Leu Ser Ala Ser
 65 70 75 80

Met Leu Asp Ile Ala Arg Ser Arg Met Pro Gly Val Pro Leu His Gln
 85 90 95

Gly Asp Met Arg Ser Phe Asp Leu Gly Pro Arg Val Ser Ala Val Thr
 100 105 110

Cys Met Phe Ser Ser Val Gly His Leu Ala Thr Thr Ala Glu Leu Asp
 115 120 125

Ala Thr Leu Arg Cys Phe Ala Arg His Thr Arg Pro Gly Gly Val Ala
 130 135 140

Val Ile Glu Pro Trp Trp Phe Pro Glu Thr Phe Thr Asp Gly Tyr Val
 145 150 155 160

Ala Gly Asp Ile Val Arg Val Asp Gly Arg Thr Ile Ser Arg Val Ser
 165 170 175

His Ser Val Arg Asp Gly Gly Ala Thr Arg Met Glu Ile His Tyr Val
 180 185 190

Ile Ala Asp Ala Glu His Gly Pro Arg His Leu Val Glu His His Arg
 195 200 205

Ile Thr Leu Phe Pro Arg His Ala Tyr Thr Ala Ala Tyr Glu Lys Ala
 210 215 220

Gly Tyr Thr Val Glu Tyr Leu Asp Gly Gly Pro Ser Gly Arg Gly Leu
225 230 235 240

Phe Val Gly Thr Arg Thr
 245

<210> 22
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 22
tcctcgatgg agacctgcc 19

<210> 23
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 23
gagaccatgc ccagggagt 19

<210> 24
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 24
tctgggagcc gtcacctt 19

<210> 25
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 25
gacgaggccg aagaggtgg 19

<210> 26

<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 26
gcacaccgga atggatgcg 19

<210> 27
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 27
ccgtcgagct ctgaggtaa 19

<210> 28
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 28
gcccgcgagccg cacgtgcgt 19

<210> 29
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 29
tgcacgcgct gctgccgacc 20

<210> 30
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 30
ttggcgaagt cgaccaggtc 20

<210> 31
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 31
gccgctcggc acggtgaact tca 23

<210> 32
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 32
atgcgcgtcg tcttctcctc catg 24

<210> 33
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 33
tcatcgtggt tctctccttc c 21

<210> 34
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 34
ggaattcatg accacgaccg atc 23

<210> 35
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 35
cgctccaggt gcaatgccgg gtgcaggc 28

<210> 36
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 36
gatcacgctc ttcgagcggc ag 22

<210> 37
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 37
gaactcgggtg gagtcgatgt c 21

<210> 38
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 38
gttgatcgatc aagacccgca c 21

<210> 39
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 39
catcgtaag gagttcgacg gt 22

<210> 40
<211> 25
<212> DNA
<213> Artificial sequence

<220>
 <223> Description of Artificial Sequence: synthetic oligonucleotide

 <400> 40
 tgcgcaggtc catgttcacc acgtt 25

 <210> 41
 <211> 20
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Description of Artificial Sequence: synthetic oligonucleotide

 <400> 41
 gctacgccct ggagagcctg 20

 <210> 42
 <211> 21
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Description of Artificial Sequence: synthetic oligonucleotide

 <400> 42
 gtcgcggtcg gagagcacga c 21

 <210> 43
 <211> 21
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Description of Artificial Sequence: synthetic oligonucleotide

 <400> 43
 gccagctcgg cgacgtccat c 21

 <210> 44
 <211> 19
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Description of Artificial Sequence: synthetic oligonucleotide

 <400> 44
 cgacgaggtc gtgcatcag 19

 <210> 45

<211> 56
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 45
aattgatcaa ggtgaacacg gtcatgcgca ggatcctcga gcggaactcc atgggg 56

<210> 46
<211> 56
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 46
ccccatggag ttccgctcga ggatcctgcg catgaccgtg ttcaccttga tcaatt 56

<210> 47
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 47
aactcggtag agtcgatgtc gtcgctgcgg aa 32

<210> 48
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 48
caatatagga aggatcaaga ggttgac 27

<210> 49
<211> 39
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<220>

<400> 49
tccggagggtg tgctgtcgga cggacttgtc ggtcggaaa 39

<210> 50
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 50
aggagcacta gtgcgggtac tgctgacgtc ctt 33

<210> 51
<211> 37
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 51
gggggatccc atatgcgggt actgctgacg tccttcg 37

<210> 52
<211> 37
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 52
gaaaagatct gccggcgtgg cggcgcgtga gttcctc 37

<210> 53
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 53
agcggcttga tcgtgttgga ccagtac 27

<210> 54
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 54
ggcctatgtg gactacgtgt tgaacgt 27

<210> 55
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 55
aacgcctcgt cctgcagcgg agacacgaac a 31

<210> 56
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 56
ttcgctcccc gatgaacaca actcgta 27

<210> 57
<211> 35
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 57
gaaggagata tacatatgcg cgtcgtcttc tcctc 35

<210> 58
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 58
cgggatcctc atcgtggttc tctccttct gc 32

<210> 59
<211> 32

<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 59
cggtaccat gcgcgtcgtc ttctcctcca tg 32

<210> 60
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 60
cggtacctc atcgtgggtc tctccttcc 29

<210> 61
<211> 13
<212> PRT
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: peptide

<400> 61
Val Thr Gly Ala Gly Asp Gly Asp Ala Asp Val Gln Ala
1 5 10